



SEQUENCE LISTING

<110> Jensen, Michael

<120> Selection Systems for Genetically Modified Cells

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<140> US/09/846,637

<141> 2001-04-30

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<301> Collart, F.R. and Huberman, E.

<302> Cloning and sequence analysis of the human and

<303> J. Biol. Chem. (1988)

<304> 263

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<301> Farazi et al.
<303> J. Biol. Chem. (1997)
<304> 271
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<303> J. Biol. Chem. (1997)
<304> 272
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<306> 961-965

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 <302> Isolation and Characterization of Mycophenolic
 <303> J. Biol. Chem. (1997)
 <304> 272
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Asp	Gly	Ile	Arg	Leu	Lys	Tyr	Arg	Gly	Met	Gly	Ser	Leu	Asp	Ala		
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aaa atc aaa gtg gcc cag gga gtg tct ggt gct gtg cag gac aaa ggg Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln Asp Lys Gly 440 445 450	1400
tca atc cac aaa ttt gtc cct tac ctg att act ggc atc caa cac tca Ser Ile His Lys Phe Val Pro Tyr Leu Ile Thr Gly Ile Gln His Ser 455 460 465	1448
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<301> Farazi et al.
<303> J. Biol. Chem. (1997)
<304> 272
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<301> Beck, J.T., Zhao, S. and Wang, C.C.
<302> Cloning, sequencing, and structural analysis of the
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Val	Phe	Arg	Lys	Asp	Tyr	Asp	Arg	Ser	Gln	Val	Cys	His	Asn	Glu	Leu	
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gtc	gat	tcg	caa	aaa	cgc	tat	ttg	gtc	gga	gca	gga	att	aac	aca	cgc	837
Val	Asp	Ser	Gln	Lys	Arg	Tyr	Leu	Val	Gly	Ala	Gly	Ile	Asn	Thr	Arg	
230							235					240				
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Asp	Phe	Arg	Glu	Arg	Val	Pro	Ala	Leu	Val	Glu	Ala	Gly	Ala	Asp	Val	
245							250					255				
ctt	tgc	att	gat	tcc	agc	gac	ggc	ttc	tca	gaa	tgg	cag	aaa	att	aca	933
Leu	Cys	Ile	Asp	Ser	Ser	Asp	Gly	Phe	Ser	Glu	Trp	Gln	Lys	Ile	Thr	
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Ile	Gly	Trp	Ile	Arg	Glu	Lys	Tyr	Gly	Asp	Lys	Val	Lys	Val	Gly	Ala	
275							280					285				
gga	aac	att	gtt	gac	ggt	gaa	gga	ttc	cgc	tat	ttg	gcc	gac	gct	gga	1029
Gly	Asn	Ile	Val	Asp	Gly	Glu	Gly	Phe	Arg	Tyr	Leu	Ala	Asp	Ala	Gly	
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gct	gat	ttc	atc	aag	att	gga	att	ggc	ggt	gga	tca	att	tgc	atc	aca	1077
Ala	Asp	Phe	Ile	Lys	Ile	Gly	Ile	Gly	Gly	Gly	Ser	Ile	Cys	Ile	Thr	
310							315					320				
cgc	gag	cag	aaa	ggt	atc	ggc	cga	ggc	caa	gct	act	gcc	gtc	att	gat	1125
Arg	Glu	Gln	Lys	Gly	Ile	Gly	Arg	Gly	Gln	Ala	Thr	Ala	Val	Ile	Asp	
325							330					335				
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Val	Val	Ala	Glu	Arg	Asn	Lys	Tyr	Phe	Glu	Glu	Thr	Gly	Ile	Tyr	Ile	
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Pro	Val	Cys	Ser	Asp	Gly	Gly	Ile	Val	Tyr	Asp	Tyr	His	Met	Thr	Leu	
355							360					365				
gct	ctt	gca	atg	ggc	gca	gat	ttc	atc	atg	ctt	ggc	agg	tac	tcc	gcc	1269
Ala	Leu	Ala	Met	Gly	Ala	Asp	Phe	Ile	Met	Leu	Gly	Arg	Tyr	Phe	Ala	
370							375					380				385
cgt	ttt	gag	gag	tca	cca	aca	aga	aaa	gtg	aca	att	aat	gga	agc	gtt	1317
Arg	Phe	Glu	Glu	Ser	Pro	Thr	Arg	Lys	Val	Thr	Ile	Asn	Gly	Ser	Val	
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atg	aag	gag	tac	tgg	gga	gaa	ggc	tct	tcg	cgc	gct	agg	aac	tgg	cag	1365
Met	Lys	Glu	Tyr	Trp	Gly	Glu	Gly	Ser	Ser	Arg	Ala	Arg	Asn	Trp	Gln	
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cgc	tat	gac	ctt	gga	ggt	aag	cag	aag	ctt	tcc	ttt	gaa	gag	gga	gtc	1413
Arg	Tyr	Asp	Leu	Gly	Gly	Lys	Gln	Lys	Leu	Ser	Phe	Glu	Glu	Gly	Val	
420							425					430				
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Asp	Ser	Tyr	Val	Pro	Tyr	Ala	Gly	Lys	Leu	Lys	Asp	Asn	Val	Glu	Ala	
435							440					445				

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Ser Leu Asn Lys Val Lys Ser Thr Met Cys Asn Cys Gly Ala Leu Thr	
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Ile Pro Gln Leu Gln Ser Lys Ala Lys Ile Thr Leu Val Ser Ser Val	
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tca att gtc gaa gga ggc gca cac gat gtt att gtt aag gac agg att	1605
Ser Ile Val Glu Gly Gly Ala His Asp Val Ile Val Lys Asp Arg Ile	
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aac gac tat cac cca aaa taaatataatt gttttatact ttatgtttgt	1653
Asn Asp Tyr His Pro Lys	
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taaattatac ctatTTactt ctcttGTTT tatgtCTTT gattCTTCCA tgtCTTTGAA	1713
ttCTTCCATG tCTTTGATT CTTTTCCCAtGatGGTGCAT GtGtGAAATT ATTCAAAACC	1773
CTTTCCCTT GtaACTTGTC AttaATTGGC AtTTCGGAG TgaACTAGTT AATTATTTT	1833
CCAATGATAT TTATTATAGT CTTTTGTGT ATTGATGTCT TACTTTACTG ATAGTgATTA	1893
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Asn	Leu	Lys	Ile	Pro	Leu	Val	Ser	Ala	Ile	Met	Gln	Ser	Val	Ser	Gly
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Glu	Lys	Met	Ala	Ile	Ala	Leu	Ala	Arg	Glu	Gly	Gly	Ile	Ser	Phe	Ile
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Phe	Gly	Ser	Gln	Ser	Ile	Glu	Ser	Gln	Ala	Ala	Met	Val	His	Ala	Val
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Lys	Asn	Phe	Lys	Ala	Gly	Phe	Val	Val	Ser	Asp	Ser	Asn	Val	Lys	Pro
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Asp	Gln	Thr	Phe	Ala	Asp	Val	Leu	Ala	Ile	Ser	Gln	Arg	Thr	Thr	His
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Gly	Leu	Val	Thr	Gln	Arg	Asp	Tyr	Pro	Ile	Asp	Leu	Thr	Gln	Thr	Glu
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Thr	Lys	Val	Ser	Asp	Met	Met	Thr	Pro	Phe	Ser	Lys	Leu	Val	Thr	Ala
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His	Gln	Asp	Thr	Lys	Leu	Ser	Glu	Ala	Asn	Lys	Ile	Ile	Trp	Glu	Lys
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Ile	Val	Phe	Arg	Lys	Asp	Tyr	Asp	Arg	Ser	Gln	Val	Cys	His	Asn	Glu
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Leu	Val	Asp	Ser	Gln	Lys	Arg	Tyr	Leu	Val	Gly	Ala	Gly	Ile	Asn	Thr
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Arg	Asp	Phe	Arg	Glu	Arg	Val	Pro	Ala	Leu	Val	Glu	Ala	Gly	Ala	Asp
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Val	Leu	Cys	Ile	Asp	Ser	Ser	Asp	Gly	Phe	Ser	Glu	Trp	Gln	Lys	Ile
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Thr	Ile	Gly	Trp	Ile	Arg	Glu	Lys	Tyr	Gly	Asp	Lys	Val	Lys	Val	Gly
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Ala	Gly	Asn	Ile	Val	Asp	Gly	Glu	Gly	Phe	Arg	Tyr	Leu	Ala	Asp	Ala
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290	295	300
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Thr Arg Glu Gln Lys Gly Ile Gly Arg Gly Gln Ala Thr Ala Val Ile		320
325	330	335
Asp Val Val Ala Glu Arg Asn Lys Tyr Phe Glu Glu Thr Gly Ile Tyr		
340	345	350
Ile Pro Val Cys Ser Asp Gly Gly Ile Val Tyr Asp Tyr His Met Thr		
355	360	365
Leu Ala Leu Ala Met Gly Ala Asp Phe Ile Met Leu Gly Arg Tyr Phe		
370	375	380
Ala Arg Phe Glu Glu Ser Pro Thr Arg Lys Val Thr Ile Asn Gly Ser		
385	390	395
Val Met Lys Glu Tyr Trp Gly Glu Ser Ser Arg Ala Arg Asn Trp		
405	410	415
Gln Arg Tyr Asp Leu Gly Gly Lys Gln Lys Leu Ser Phe Glu Glu Gly		
420	425	430
Val Asp Ser Tyr Val Pro Tyr Ala Gly Lys Leu Lys Asp Asn Val Glu		
435	440	445
Ala Ser Leu Asn Lys Val Lys Ser Thr Met Cys Asn Cys Gly Ala Leu		
450	455	460
Thr Ile Pro Gln Leu Gln Ser Lys Ala Lys Ile Thr Leu Val Ser Ser		
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Ile Asn Asp Tyr His Pro Lys		
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		15

ctg ggt ggt tgt cgc cgt ctc cca cta acc tgc aga caa ctt cga ttc		96
Leu Gly Gly Cys Arg Arg Leu Pro Leu Thr Cys Arg Gln Leu Arg Phe		
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gcc tcc gac agc gga gcc gca gcg gca act aca aaa gca acg gcc gaa		144
Ala Ser Asp Ser Gly Ala Ala Ala Thr Thr Lys Ala Thr Ala Glu		
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tca gca gcc gag tca gct agt ata aac gtc aaa gag gca ccc aaa aag		192
Ser Ala Ala Glu Ser Ala Ser Ile Asn Val Lys Glu Ala Pro Lys Lys		
50	55	60

gcc gga cgg ggc ctg cgg cgc acg gtc ctg gga acg tcg ttg gcg ctg		240
Ala Gly Arg Gly Leu Arg Arg Thr Val Leu Gly Thr Ser Leu Ala Leu		
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		80

acg ctg ctg gtt gga tat gtc tac ggg acg gac acc cgg gcg agt gtg		288
Thr Leu Leu Val Gly Tyr Val Tyr Gly Thr Asp Thr Arg Ala Ser Val		
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cat cgg tac ggt gtt gtg ccg ctg att aga gca ttg tat cct gat gcg		336
His Arg Tyr Gly Val Val Pro Leu Ile Arg Ala Leu Tyr Pro Asp Ala		
100	105	110

gaa	gat	gcf	cat	cat	att	ggt	gtc	gat	act	tta	aag	atg	ctg	tat	aag	384
Glu	Asp	Ala	His	His	Ile	Gly	Val	Asp	Thr	Leu	Lys	Met	Leu	Tyr	Lys	
115							120					125				
tat	ggt	ctg	cat	cca	agg	gaa	cgf	ggg	gat	ccg	gat	gga	gat	ggg	gcf	432
Tyr	Gly	Leu	His	Pro	Arg	Glu	Arg	Gly	Asp	Pro	Asp	Gly	Asp	Gly	Ala	
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ctg	gcf	aca	gag	gtc	ttt	ggg	tat	aca	ctg	tca	aac	cca	att	ggc	ata	480
Leu	Ala	Thr	Glu	Val	Phe	Gly	Tyr	Thr	Leu	Ser	Asn	Pro	Ile	Gly	Ile	
145						150				155				160		
tcg	ggc	ggc	ctg	gac	aag	cat	gct	gag	atc	cct	gat	ccg	ctg	tcc	gcf	528
Ser	Gly	Gly	Leu	Asp	Lys	His	Ala	Glu	Ile	Pro	Asp	Pro	Leu	Phe	Ala	
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Ile	Gly	Pro	Ala	Ile	Val	Glu	Val	Gly	Gly	Thr	Thr	Pro	Leu	Pro	Gln	
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Asp	Gly	Asn	Pro	Arg	Pro	Arg	Val	Phe	Arg	Leu	Pro	Ser	Gln	Arg	Ala	
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Met	Ile	Asn	Arg	Tyr	Gly	Leu	Asn	Ser	Lys	Gly	Ala	Asp	His	Met	Ala	
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Ala	Ile	Leu	Glu	Gln	Arg	Val	Arg	Asp	Phe	Ala	Tyr	Ala	Asn	Gly	Phe	
225						230				235				240		
ggg	gca	tac	gat	gcf	gct	aag	cag	cgt	gta	ttg	gac	ggc	gaa	gct	ggt	768
Gly	Ala	Tyr	Asp	Ala	Ala	Lys	Gln	Arg	Val	Leu	Asp	Gly	Glu	Ala	Gly	
245							250					255				
gtg	cca	cca	ggt	agt	ctt	cag	cct	ggt	aag	ctt	tta	gct	gtc	caa	gtg	816
Val	Pro	Pro	Gly	Ser	Leu	Gln	Pro	Gly	Lys	Leu	Leu	Ala	Val	Gln	Val	
260						265					270					
gca	aag	aac	aag	gcc	act	cct	gac	ggc	gac	att	gaa	gcc	atc	aag	cgc	864
Ala	Lys	Asn	Lys	Ala	Thr	Pro	Asp	Gly	Asp	Ile	Glu	Ala	Ile	Lys	Arg	
275						280					285					
gac	tat	gtg	tat	tgc	gtg	gac	cgt	gtg	gcc	aaa	tac	gct	gat	att	ctt	912
Asp	Tyr	Val	Tyr	Cys	Val	Asp	Arg	Val	Ala	Lys	Tyr	Ala	Asp	Ile	Leu	
290						295				300						
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Val	Val	Asn	Val	Ser	Ser	Pro	Asn	Thr	Pro	Gly	Leu	Arg	Asp	Leu	Gln	
305						310				315				320		
gcc	act	gcc	ccg	ctc	aca	gct	atc	ttg	agt	gct	gtc	gtt	ggc	gcf	gca	1008
Ala	Thr	Ala	Pro	Leu	Thr	Ala	Ile	Leu	Ser	Ala	Val	Val	Gly	Ala	Ala	
325							330					335				
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Lys	Ser	Val	Asn	Arg	Lys	Thr	Lys	Pro	Tyr	Val	Met	Val	Lys	Val	Ser	
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Pro	Asp	Glu	Asp	Ser	Asp	Glu	Gln	Val	Ser	Gly	Ile	Cys	Asp	Ala	Val	
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cga	gca	tcc	ggt	gtc	gac	gga	gtg	att	gtc	gga	aac	aca	aca	aac	cgt	1152
Arg	Ala	Ser	Gly	Val	Asp	Gly	Val	Ile	Val	Gly	Asn	Thr	Thr	Asn	Arg	
370							375					380				

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Arg Pro Asp Pro Ile Pro Gln Gly Tyr Thr Leu Pro Ala Lys Glu Gln			
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gca acg ttg aaa gaa acc ggc ggg tat tca ggt cca cag ctg ttc gat	1248		
Ala Thr Leu Lys Glu Thr Gly Gly Tyr Ser Gly Pro Gln Leu Phe Asp			
405	410	415	
cgc aca gtg gcc ctt gtg gct cgg tac cgc tcc atg ctg gat gcg gag	1296		
Arg Thr Val Ala Leu Val Ala Arg Tyr Arg Ser Met Leu Asp Ala Glu			
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tcg gaa acg gcc gga tcc gcc aag gat tca gca gcg acc ata gcg caa	1344		
Ser Glu Thr Ala Gly Ser Ala Lys Asp Ser Ala Ala Thr Ile Ala Gln			
435	440	445	
aca gag cca ggc tcg gaa aac gtt cct cct gtg gaa gcg cca agc gga	1392		
Thr Glu Pro Gly Ser Glu Asn Val Pro Pro Val Glu Ala Pro Ser Gly			
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ctg ccg cgc aaa gtt atc ttc gct tcg ggt ggt atc acc aac ggg aag	1440		
Leu Pro Arg Lys Val Ile Phe Ala Ser Gly Gly Ile Thr Asn Gly Lys			
465	470	475	480
cag gct cac gct gtt tta gac aca ggg gca tct gtt gcc atg atg tac	1488		
Gln Ala His Ala Val Leu Asp Thr Gly Ala Ser Val Ala Met Met Tyr			
485	490	495	
acc ggt gtg gtc tat ggt ggc gtc ggc act gtc act cga gtg aag caa	1536		
Thr Gly Val Val Tyr Gly Gly Val Gly Thr Val Thr Arg Val Lys Gln			
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gaa ctt cga acg gcg aaa aag gag	1560		
Glu Leu Arg Thr Ala Lys Lys Glu			
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 35 40 45
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 Ala Gly Arg Gly Leu Arg Arg Thr Val Leu Gly Thr Ser Leu Ala Leu
 65 70 75 80
 Thr Leu Leu Val Gly Tyr Val Tyr Gly Thr Asp Thr Arg Ala Ser Val
 85 90 95
 His Arg Tyr Gly Val Val Pro Leu Ile Arg Ala Leu Tyr Pro Asp Ala
 100 105 110
 Glu Asp Ala His His Ile Gly Val Asp Thr Leu Lys Met Leu Tyr Lys
 115 120 125
 Tyr Gly Leu His Pro Arg Glu Arg Gly Asp Pro Asp Gly Asp Gly Ala
 130 135 140
 Leu Ala Thr Glu Val Phe Gly Tyr Thr Leu Ser Asn Pro Ile Gly Ile
 145 150 155 160
 Ser Gly Gly Leu Asp Lys His Ala Glu Ile Pro Asp Pro Leu Phe Ala
 165 170 175
 Ile Gly Pro Ala Ile Val Glu Val Gly Gly Thr Thr Pro Leu Pro Gln

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Asp	Tyr	Val	Tyr	Cys	Val	Asp	Arg	Val	Ala	Lys	Tyr	Ala	Asp	Ile	Leu
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Pro	Asp	Glu	Asp	Ser	Asp	Glu	Gln	Val	Ser	Gly	Ile	Cys	Asp	Ala	Val
							355					360			365

Arg	Ala	Ser	Gly	Val	Asp	Gly	Val	Ile	Val	Gly	Asn	Thr	Thr	Asn	Arg
370							375					380			
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Ala	Thr	Leu	Lys	Glu	Thr	Gly	Gly	Tyr	Ser	Gly	Pro	Gln	Leu	Phe	Asp
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Arg	Thr	Val	Ala	Leu	Val	Ala	Arg	Tyr	Arg	Ser	Met	Leu	Asp	Ala	Glu
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Ser	Glu	Thr	Ala	Gly	Ser	Ala	Lys	Asp	Ser	Ala	Ala	Thr	Ile	Ala	Gln
							435					440			445
Thr	Glu	Pro	Gly	Ser	Glu	Asn	Val	Pro	Pro	Val	Glu	Ala	Pro	Ser	Gly
							450					455			460
Leu	Pro	Arg	Lys	Val	Ile	Phe	Ala	Ser	Gly	Gly	Ile	Thr	Asn	Gly	Lys
465							470					475			480
Gln	Ala	His	Ala	Val	Leu	Asp	Thr	Gly	Ala	Ser	Val	Ala	Met	Met	Tyr
							485					490			495
Thr	Gly	Val	Val	Tyr	Gly	Gly	Val	Gly	Thr	Val	Thr	Arg	Val	Lys	Gln
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Glu	Leu	Arg	Thr	Ala	Lys	Lys	Glu								
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CDS
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 <222> (601)...(2142)
 <223> Human wild-type IMPDH type I

<300>
 <301> Natsumeda et al.
 <302> Two Distinct cDNAs for Human IMP Dehydrogenase
 <303> J. Biol. Chem. (1990)
 <304> 265
 <305> 9
 <306> 5292-5295

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Ser	Gly	Gly	Thr	Gly	Tyr	
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Gly	Leu	Thr	Ala	Gln	Gln	
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				Ala	Ser	
				Asp	Asp	
				Leu	Thr	Tyr
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Asn	Asp	Phe	Leu	Ile	Leu	
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				Phe	Ile	
				Asp	Asp	
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gtg	gac	ctg	acc	tca	gcc	792
Val	Asp	Leu	Thr	Ser	Ala	
				Leu	Thr	
				Arg	Lys	
50	55	60				
ctc	atc	tcc	tcc	ccc	atg	840
Leu	Ile	Ser	Ser	Pro	Met	
				Asp	Thr	
				Val	Thr	
65	70	75				
gcc	atg	gct	ctg	atg	gga	888
Ala	Met	Ala	Leu	Met	Gly	
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				Ile	Gly	
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cca	gag	ttc	cag	gcc	aat	936
Pro	Glu	Phe	Gln	Ala	Asn	
				Glu	Val	
				Arg	Lys	
100	105	110				
ggc	ttc	atc	acg	gac	cct	984
Gly	Phe	Ile	Thr	Asp	Pro	
				Val	Val	
				Leu	Ser	
115	120	125				
gat	gtg	ctg	gag	gcc	aag	1032
Asp	Val	Leu	Glu	Ala	Lys	
				Met	Arg	
				Gly	Phe	
130	135	140				
act	gag	acg	ggc	acc	atg	1080
Thr	Glu	Thr	Gly	Thr	Met	
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145	150	155				
cga	gac	atc	gac	ttt	ctt	1128
Arg	Asp	Ile	Asp	Phe	Leu	
				Ala	Glu	
				Lys	Lys	
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gag	gtg	atg	acg	cca	agg	1176
Glu	Val	Met	Thr	Pro	Arg	
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				Glu	Glu	
180	185	190				
acg	ttg	aaa	gag	gca	aat	1224
Thr	Leu	Lys	Glu	Ala	Asn	
				Glu	Ile	
				Arg	Gln	
195	200	205				
ctg	cct	atc	gtc	aat	gat	1272
Leu	Pro	Ile	Val	Asn	Asp	
				Cys	Asp	
				Asp	Glu	
210	215	220				
acc	gac	ctg	aag	aag	aat	1320
Thr	Asp	Leu	Lys	Lys	Asn	
				Arg	Tyr	
225	230	235				
cag	aag	cag	ctg	ctc	tgt	1368

Gln	Lys	Gln	Leu	Leu	Cys	Gly	Ala	Ala	Val	Gly	Thr	Arg	Glu	Asp	Asp	
					245				250				255			
aaa	tac	cgt	ctg	gac	ctg	ctg	acc	cag	gcg	ggg	gtc	gac	gtc	ata	gtc	1416
Lys	Tyr	Arg	Leu	Asp	Leu	Leu	Thr	Gln	Ala	Gly	Val	Asp	Val	Ile	Val	
					260				265				270			
ttc	cac	tcg	tcc	caa	ggg	aat	tcg	gtg	tat	cag	atc	gcc	atg	gtg	cat	1464
Phe	His	Ser	Ser	Gln	Gly	Asn	Ser	Val	Tyr	Gln	Ile	Ala	Met	Val	His	
					275				280				285			
tac	atc	aaa	cag	aag	tac	ccc	cac	ctc	cag	gtg	att	ggg	ggg	aac	gtg	1512
Tyr	Ile	Lys	Gln	Lys	Tyr	Pro	His	Leu	Gln	Val	Ile	Gly	Gly	Asn	Val	
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gtg	aca	gca	gcc	cag	gcc	aag	aac	ctg	att	gat	gct	ggt	gtg	gac	ggg	1560
Val	Thr	Ala	Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	Asp	Gly	
					305				310				315			320
ctg	cgc	gtg	ggc	atg	ggc	tgc	ggc	tcc	atc	tgc	atc	acc	cag	gaa	gtg	1608
Leu	Arg	Val	Gly	Met	Gly	Cys	Gly	Ser	Ile	Cys	Ile	Thr	Gln	Glu	Val	
					325				330						335	
atg	gcc	tgt	ggt	cgg	ccc	cag	ggc	act	gct	gtg	tac	aag	gtg	gtt	gag	1656
Met	Ala	Cys	Gly	Arg	Pro	Gln	Gly	Thr	Ala	Val	Tyr	Lys	Val	Ala	Glu	
					340				345				350			
tat	gcc	cgg	cgc	ttt	ggt	gtg	ccc	atc	ata	gcc	gat	ggc	ggc	atc	cag	1704
Tyr	Ala	Arg	Arg	Phe	Gly	Val	Pro	Ile	Ile	Ala	Asp	Gly	Gly	Ile	Gln	
					355				360				365			
acc	gtg	gga	cac	gtg	gtc	aag	gcc	ctg	gcc	ctt	gga	gcc	tcc	aca	gtg	1752
Thr	Val	Gly	His	Val	Val	Lys	Ala	Leu	Ala	Leu	Gly	Ala	Ser	Thr	Val	
					370				375				380			
atg	atg	ggc	tcc	ctg	ctg	gcc	gcc	act	acg	gag	gcc	cct	ggc	gag	tac	1800
Met	Met	Gly	Ser	Leu	Leu	Ala	Ala	Thr	Thr	Glu	Ala	Pro	Gly	Glu	Tyr	
					385				390				395			400
ttc	ttc	tca	gac	ggg	gtg	cgg	ctc	aag	aag	tac	cgg	ggc	atg	ggc	tca	1848
Phe	Phe	Ser	Asp	Gly	Val	Arg	Leu	Lys	Lys	Tyr	Arg	Gly	Met	Gly	Ser	
					405				410						415	
ctg	gat	ccc	atg	gag	aag	agc	agc	agc	agc	cag	aaa	cga	tac	ttc	agc	1896
Leu	Asp	Pro	Met	Glu	Lys	Ser	Ser	Ser	Ser	Gln	Lys	Arg	Tyr	Phe	Ser	
					420				425				430			
gag	ggg	gat	aaa	gtg	aag	atc	gca	cag	ggt	gtc	tcg	ggc	tcc	atc	cag	1944
Glu	Gly	Asp	Lys	Val	Lys	Ile	Ala	Gln	Gly	Val	Ser	Gly	Ser	Ile	Gln	
					435				440				445			
gac	aaa	gga	tcc	att	cag	aag	ttc	gtg	ccc	tac	ctc	ata	gca	ggc	atc	1992
Asp	Lys	Gly	Ser	Ile	Gln	Lys	Phe	Val	Pro	Tyr	Leu	Ile	Ala	Gly	Ile	
					450				455				460			
caa	cac	ggc	tgc	cag	gat	atc	ggg	gcc	cgc	agc	ctg	tct	gtc	ctt	cg	2040
Gln	His	Gly	Cys	Gln	Asp	Ile	Gly	Ala	Arg	Ser	Leu	Ser	Val	Leu	Arg	
					465				470				475			480
tcc	atg	atg	tac	tca	gga	gag	ctc	aag	ttt	gag	aag	cgg	acc	atg	tcg	2088
Ser	Met	Met	Tyr	Ser	Gly	Glu	Leu	Lys	Phe	Glu	Lys	Arg	Thr	Met	Ser	
					485				490						495	
ccc	cag	att	gag	ggt	gtc	cat	ggc	ctg	cac	tct	tac	gaa	aag	cgg	2136	
Pro	Gln	Ile	Glu	Gly	Gly	Val	His	Gly	Leu	His	Ser	Tyr	Glu	Lys	Arg	
					500				505				510			

ctg tac tgaggacagc ggtggaggcc gaggtggtgg agggatgca cccagtgca
Leu Tyr

2192

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tcaccaccgt cccaggtga accattcctc cttctccctc agctgcagtc gaaggctta 2792
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gcaggt 2858

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<212> PRT
<213> Homo sapien

<400> 18

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				20				25					30		
Asn	Asp	Phe	Leu	Ile	Leu	Pro	Gly	Phe	Ile	Asp	Phe	Ile	Ala	Asp	Glu
						35		40				45			
Val	Asp	Leu	Thr	Ser	Ala	Leu	Thr	Arg	Lys	Ile	Thr	Leu	Lys	Thr	Pro
						50		55			60				
Leu	Ile	Ser	Ser	Pro	Met	Asp	Thr	Val	Thr	Glu	Ala	Asp	Met	Ala	Ile
					65		70		75				80		
Ala	Met	Ala	Leu	Met	Gly	Gly	Ile	Gly	Phe	Ile	His	His	Asn	Cys	Thr
						85		90				95			
Pro	Glu	Phe	Gln	Ala	Asn	Glu	Val	Arg	Lys	Val	Lys	Asn	Phe	Glu	Gln
						100		105				110			
Gly	Phe	Ile	Thr	Asp	Pro	Val	Val	Leu	Ser	Pro	Ser	His	Thr	Val	Gly
						115		120			125				
Asp	Val	Leu	Glu	Ala	Lys	Met	Arg	His	Gly	Phe	Ser	Gly	Ile	Pro	Ile
						130		135			140				
Thr	Glu	Thr	Gly	Thr	Met	Gly	Ser	Lys	Leu	Val	Gly	Ile	Val	Thr	Ser
					145		150			155			160		
Arg	Asp	Ile	Asp	Phe	Leu	Ala	Glu	Lys	Asp	His	Thr	Thr	Leu	Leu	Ser
						165		170			175				
Glu	Val	Met	Thr	Pro	Arg	Ile	Glu	Leu	Val	Val	Ala	Pro	Ala	Gly	Val
						180		185			190				
Thr	Leu	Lys	Glu	Ala	Asn	Glu	Ile	Leu	Gln	Arg	Ser	Lys	Lys	Gly	Lys
						195		200			205				
Leu	Pro	Ile	Val	Asn	Asp	Cys	Asp	Glu	Leu	Val	Ala	Ile	Ile	Ala	Arg
						210		215			220				
Thr	Asp	Leu	Lys	Lys	Asn	Arg	Asp	Tyr	Pro	Leu	Ala	Ser	Lys	Asp	Ser
						225		230			235			240	
Gln	Lys	Gln	Leu	Leu	Cys	Gly	Ala	Ala	Val	Gly	Thr	Arg	Glu	Asp	Asp
						245		250			255				
Lys	Tyr	Arg	Leu	Asp	Leu	Leu	Thr	Gln	Ala	Gly	Val	Asp	Val	Ile	Val
						260		265			270				
Phe	His	Ser	Ser	Gln	Gly	Asn	Ser	Val	Tyr	Gln	Ile	Ala	Met	Val	His
						275		280			285				
Tyr	Ile	Lys	Gln	Lys	Tyr	Pro	His	Leu	Gln	Val	Ile	Gly	Gly	Asn	Val
						290		295			300				
Val	Thr	Ala	Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	Asp	Gly
						305		310			315			320	
Leu	Arg	Val	Gly	Met	Gly	Cys	Gly	Ser	Ile	Cys	Ile	Thr	Gln	Glu	Val
						325		330			335				
Met	Ala	Cys	Gly	Arg	Pro	Gln	Gly	Thr	Ala	Val	Tyr	Lys	Val	Ala	Glu
						340		345			350				

Tyr Ala Arg Arg Phe Gly Val Pro Ile Ile Ala Asp Gly Gly Ile Gln
 355 360 365
 Thr Val Gly His Val Val Lys Ala Leu Ala Leu Gly Ala Ser Thr Val
 370 375 380
 Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr
 385 390 395 400
 Phe Phe Ser Asp Gly Val Arg Leu Lys Tyr Arg Gly Met Gly Ser
 405 410 415
 Leu Asp Pro Met Glu Lys Ser Ser Ser Gln Lys Arg Tyr Phe Ser
 420 425 430
 Glu Gly Asp Lys Val Lys Ile Ala Gln Gly Val Ser Gly Ser Ile Gln
 435 440 445
 Asp Lys Gly Ser Ile Gln Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile
 450 455 460
 Gln His Gly Cys Gln Asp Ile Gly Ala Arg Ser Leu Ser Val Leu Arg
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 485 490 495
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 Leu Tyr

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<300>
 <301> Minet, M., Dufour, M-E., and Lacroute, F.
 <302> Cloning and Sequencing of a Human cDNA coding for
 <303> Gene (1992)
 <304> 121
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<400> 19

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atc ctg ggg gga gga ctt ctc ttc gcc tcc tac ctg atg gcc acg	96
Ile Leu Gly Gly Gly Leu Leu Phe Ala Ser Tyr Leu Met Ala Thr	
20 25 30	
gga gat gag cgt ttc tat gct gaa cac ctg atg ccg act ctg cag ggg	144
Gly Asp Glu Arg Phe Tyr Ala Glu His Leu Met Pro Thr Leu Gln Gly	
35 40 45	
ctg ctg gac ccg gag tca gcc cac aga ctg gct gtt cgc ttc acc tcc	192
Leu Leu Asp Pro Glu Ser Ala His Arg Leu Ala Val Arg Phe Thr Ser	
50 55 60	
ctg ggg ctc ctt cca cgg gcc aga ttt caa gac tct gac atg ctg gaa	240
Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp Met Leu Glu	
65 70 75 80	
gtg aga gtt ctg ggc cat aaa ttc cga aat cca gta gga att gct gca	288
Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly Ile Ala Ala	
85 90 95	
gga ttt gac aag cat ggg gaa gcc gtg gac gga ctt tat aag atg ggc	336

Gly	Phe	Asp	Lys	His	Gly	Glu	Ala	Val	Asp	Gly	Leu	Tyr	Lys	Met	Gly	
100					105								110			
ttt	ggt	ttt	gtt	gag	ata	gga	agt	gtg	act	cca	aaa	cct	cag	gaa	gga	384
Phe	Gly	Phe	Val	Glu	Ile	Gly	Ser	Val	Thr	Pro	Lys	Pro	Gln	Glu	Gly	
115					120							125				
aac	cct	aga	ccc	aga	gtc	tcc	cgc	ctc	cct	gag	gac	caa	gct	gtc	att	432
Asn	Pro	Arg	Pro	Arg	Val	Phe	Arg	Leu	Pro	Glu	Asp	Gln	Ala	Val	Ile	
130					135						140					
aac	agg	tat	gga	ttt	aac	agt	cac	ggg	ctt	tca	gtg	gtg	gaa	cac	agg	480
Asn	Arg	Tyr	Gly	Phe	Asn	Ser	His	Gly	Leu	Ser	Val	Val	Glu	His	Arg	
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Leu	Arg	Ala	Arg	Gln	Gln	Lys	Gln	Ala	Lys	Leu	Thr	Glu	Asp	Gly	Leu	
165					170						175					
cct	ctg	ggg	gtc	aac	ttg	ggg	aag	aac	aag	acc	tca	gtg	gac	gcc	g	576
Pro	Leu	Gly	Val	Asn	Leu	Gly	Lys	Asn	Lys	Thr	Ser	Val	Asp	Ala	Ala	
180					185						190					
gag	gac	tac	gca	gaa	ggg	gtg	cg	gt	ctg	ggc	ccc	ctg	gcc	gac	tac	824
Glu	Asp	Tyr	Ala	Glu	Gly	Val	Arg	Val	Leu	Gly	Pro	Leu	Ala	Asp	Tyr	
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Leu	Val	Val	Asn	Val	Ser	Ser	Pro	Asn	Thr	Ala	Gly	Leu	Arg	Ser	Leu	
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cag	gga	aag	gcc	gag	ctg	cg	cg	ctg	ctg	acc	aag	gt	ctg	cag	gag	720
Gln	Gly	Lys	Ala	Glu	Leu	Arg	Arg	Leu	Leu	Thr	Lys	Val	Leu	Gln	Glu	
225					230						235		240			
agg	gat	ggc	ttg	cg	aga	gt	cac	agg	ccg	gca	gt	ctg	gt	aag	atc	768
Arg	Asp	Gly	Leu	Arg	Arg	Val	His	Arg	Pro	Ala	Val	Leu	Val	Lys	Ile	
245					250						255					
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Ala	Pro	Asp	Leu	Thr	Ser	Gln	Asp	Lys	Glu	Asp	Ile	Ala	Ser	Val	Val	
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Lys	Glu	Leu	Gly	Ile	Asp	Gly	Leu	Ile	Val	Thr	Asn	Thr	Thr	Val	Ser	
275					280						285					
cgc	cct	gc	ggc	ctc	cag	gg	gc	ctg	cg	tct	gaa	aca	gga	gg	ctg	912
Arg	Pro	Ala	Gly	Leu	Gln	Gly	Ala	Leu	Arg	Ser	Glu	Thr	Gly	Gly	Leu	
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Ser	Gly	Lys	Pro	Leu	Arg	Asp	Leu	Ser	Thr	Gln	Thr	Ile	Arg	Glu	Met	
305					310						315		320			
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Tyr	Ala	Leu	Thr	Gln	Gly	Arg	Val	Pro	Ile	Ile	Gly	Val	Gly	Gly	Val	
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Ser	Ser	Gly	Gln	Asp	Ala	Leu	Glu	Lys	Ile	Arg	Ala	Gly	Ala	Ser	Leu	
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gt	cag	ctg	tac	acg	gc	ctc	acc	tcc	tgg	ggg	cca	ccc	gtt	gt	gg	1104
Val	Gln	Leu	Tyr	Thr	Ala	Leu	Thr	Phe	Trp	Gly	Pro	Pro	Val	Val	Gly	
355					360						365					

aaa gtc aag cgg gaa ctg gag gcc ctt ctg aaa gag cag ggc ttt ggc 1152
 Lys Val Lys Arg Glu Leu Glu Ala Leu Leu Lys Glu Gln Gly Phe Gly
 370 375 380

gga gtc aca gat gcc att gga gca gat cat cg^g agg tgaggacagc 1198
 Gly Val Thr Asp Ala Ile Gly Ala Asp His Arg Arg
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 35 40 45

Leu Leu Asp Pro Glu Ser Ala His Arg Leu Ala Val Arg Phe Thr Ser
 50 55 60

Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp Met Leu Glu
 65 70 75 80

Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly Ile Ala Ala
 85 90 95

Gly Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr Lys Met Gly
 100 105 110

Phe Gly Phe Val Glu Ile Gly Ser Val Thr Pro Lys Pro Gln Glu Gly
 115 120 125

Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln Ala Val Ile
 130 135 140

Asn Arg Tyr Gly Phe Asn Ser His Gly Leu Ser Val Val Glu His Arg
 145 150 155 160

Leu Arg Ala Arg Gln Gln Lys Gln Ala Lys Leu Thr Glu Asp Gly Leu
 165 170 175

Pro Leu Gly Val Asn Leu Gly Lys Asn Lys Thr Ser Val Asp Ala Ala
 180 185 190

Glu Asp Tyr Ala Glu Gly Val Arg Val Leu Gly Pro Leu Ala Asp Tyr
 195 200 205

Leu Val Val Asn Val Ser Ser Pro Asn Thr Ala Gly Leu Arg Ser Leu
 210 215 220

Gln Gly Lys Ala Glu Leu Arg Arg Leu Leu Thr Lys Val Leu Gln Glu
 225 230 235 240

Arg Asp Gly Leu Arg Arg Val His Arg Pro Ala Val Leu Val Lys Ile
 245 250 255

Ala Pro Asp Leu Thr Ser Gln Asp Lys Glu Asp Ile Ala Ser Val Val
 260 265 270

Lys Glu Leu Gly Ile Asp Gly Leu Ile Val Thr Asn Thr Thr Val Ser
 275 280 285

Arg Pro Ala Gly Leu Gln Gly Ala Leu Arg Ser Glu Thr Gly Gly Leu
 290 295 300

Ser Gly Lys Pro Leu Arg Asp Leu Ser Thr Gln Thr Ile Arg Glu Met
 305 310 315 320

Tyr Ala Leu Thr Gln Gly Arg Val Pro Ile Ile Gly Val Gly Val
 325 330 335

Ser Ser Gly Gln Asp Ala Leu Glu Lys Ile Arg Ala Gly Ala Ser Leu
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Val Gln Leu Tyr Thr Ala Leu Thr Phe Trp Gly Pro Pro Val Val Gly
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Lys Val Lys Arg Glu Leu Glu Ala Leu Leu Lys Glu Gln Gly Phe Gly

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<300>			
<301> Copeland, R.A., et al.			
<302> Recombinant Human Dihydroorotate Dehydrogenase			
<303> Arch. Biochem. Biophys. (1995)			
<304> 323			
<306> 79-86			
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Met Ala Thr Gly Asp Glu Arg Phe Tyr Ala Glu His Leu Met Pro Thr			
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ctg cag ggg ctg ctg gac ccg gag tca gcc cac aga ctg gct gtt cgc			96
Leu Gln Gly Leu Leu Asp Pro Glu Ser Ala His Arg Leu Ala Val Arg			
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ttc acc tcc ctg ggg ctc ctt cca cggtt ccc aga ttt caa gac tct gac			144
Phe Thr Ser Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp			
35	40	45	
atg ctg gaa gtg aga gtt ctg ggc cat aaa ttc cga aat cca gta gga			192
Met Leu Glu Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly			
50	55	60	
att gct gca gga ttt gac aag cat ggg gaa gcc gtg gac gga ctt tat			240
Ile Ala Ala Gly Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr			
65	70	75	80
aag atg ggc ttt ggt ttt gtt gag ata gga agt gtg act cca aaa cct			288
Lys Met Gly Phe Gly Phe Val Glu Ile Gly Ser Val Thr Pro Lys Pro			
85	90	95	
cag gaa gga aac cct aga ccc aga gtc ttc cgc ctc cct gag gac caa			336
Gln Glu Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln			
100	105	110	
gct gtc att aac agg tat gga ttt aac agt cac ggg ctt tca gtg gtg			384
Ala Val Ile Asn Arg Tyr Gly Phe Asn Ser His Gly Leu Ser Val Val			
115	120	125	
gaa cac agg tta cgg gcc aga cag cag aag cag gcc aag ctc aca gaa			432
Glu His Arg Leu Arg Ala Arg Gln Gln Lys Gln Ala Lys Leu Thr Glu			
130	135	140	
gat gga ctg cct ctg ggg gtc aac ttg ggg aag aac aag acc tca gtg			480
Asp Gly Leu Pro Leu Gly Val Asn Leu Gly Lys Asn Lys Thr Ser Val			
145	150	155	160
gac gcc gcg gag gac tac gca gaa ggg gtg cgc gta ctg ggc ccc ctg			528
Asp Ala Ala Glu Asp Tyr Ala Glu Gly Val Arg Val Leu Gly Pro Leu			
165	170	175	
gcc gac tac ctg gtg aat gtg tcc agc ccc aac act gcc ggg ctg			576

Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Ala Gly Leu	180	185	190	
cgg agc ctt cag gga aag gcc gag ctg cgc cgc ctg ctg acc aag gtg	195	200	205	624
Arg Ser Leu Gln Gly Lys Ala Glu Leu Arg Arg Leu Leu Thr Lys Val				
ctg cag gag agg gat ggc ttg cgg aga gtg cac agg ccg gca gtc ctg	210	215	220	672
Leu Gln Glu Arg Asp Gly Leu Arg Arg Val His Arg Pro Ala Val Leu				
gtg aag atc gct cct gac ctc acc agc cag gat aag gag gac att gcc	225	230	235	720
Val Lys Ile Ala Pro Asp Leu Thr Ser Gln Asp Lys Glu Asp Ile Ala				
agt gtg gtc aaa gag ttg ggc atc gat ggg ctg att gtt acg aac acc	245	250	255	768
Ser Val Val Lys Glu Leu Gly Ile Asp Gly Leu Ile Val Thr Asn Thr				
acc gtg agt cgc cct gcg ggc ctc cag ggt gcc ctg cgc tct gaa aca	260	265	270	816
Thr Val Ser Arg Pro Ala Gly Leu Gln Gly Ala Leu Arg Ser Glu Thr				
gga ggg ctg agt ggg aag ccc ctc cgg gat tta tca act caa acc att	275	280	285	864
Gly Gly Leu Ser Gly Lys Pro Leu Arg Asp Leu Ser Thr Gln Thr Ile				
cgg gag atg tat gca ctc acc caa ggc cga gtt ccc ata att ggg gtt	290	295	300	912
Arg Glu Met Tyr Ala Leu Thr Gln Gly Arg Val Pro Ile Ile Gly Val				
ggt ggt gtg agc agc ggg cag gac gcg ctg gag aag atc cgg gca ggg	305	310	315	960
Gly Gly Val Ser Ser Gly Gln Asp Ala Leu Glu Lys Ile Arg Ala Gly				
gcc tcc ctg gtg cag ctg tac acg gcc ctc acc ttc tgg ggg cca ccc	325	330	335	1008
Ala Ser Leu Val Gln Leu Tyr Thr Ala Leu Thr Phe Trp Gly Pro Pro				
gtt gtg ggc aaa gtc aag cgg gaa ctg gag gcc ctt ctg aaa gag cag	340	345	350	1056
Val Val Gly Lys Val Lys Arg Glu Leu Glu Ala Leu Leu Lys Glu Gln				
ggc ttt ggc gga gtc aca gat gcc att gga gca gat cat cgg agg	355	360	365	1101
Gly Phe Gly Gly Val Thr Asp Ala Ile Gly Ala Asp His Arg Arg				
<210> 22				
<211> 367				
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<213> Homo sapien				
<400> 22				
Met Ala Thr Gly Asp Glu Arg Phe Tyr Ala Glu His Leu Met Pro Thr	1	5	10	15
Leu Gln Gly Leu Leu Asp Pro Glu Ser Ala His Arg Leu Ala Val Arg	20	25	30	
Phe Thr Ser Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp	35	40	45	
Met Leu Glu Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly	50	55	60	
Ile Ala Ala Gly Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr	65	70	75	80
Lys Met Gly Phe Gly Phe Val Glu Ile Gly Ser Val Thr Pro Lys Pro	85	90	95	
Gln Glu Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln				

100	105	110
Ala Val Ile Asn Arg Tyr Gly Phe Asn Ser His Gly Leu Ser Val Val		
115	120	125
Glu His Arg Leu Arg Ala Arg Gln Gln Lys Gln Ala Lys Leu Thr Glu		
130	135	140
Asp Gly Leu Pro Leu Gly Val Asn Leu Gly Lys Asn Lys Thr Ser Val		
145	150	155
Asp Ala Ala Glu Asp Tyr Ala Glu Gly Val Arg Val Leu Gly Pro Leu		160
165	170	175
Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Ala Gly Leu		
180	185	190
Arg Ser Leu Gln Gly Lys Ala Glu Leu Arg Arg Leu Leu Thr Lys Val		
195	200	205
Leu Gln Glu Arg Asp Gly Leu Arg Arg Val His Arg Pro Ala Val Leu		
210	215	220
Val Lys Ile Ala Pro Asp Leu Thr Ser Gln Asp Lys Glu Asp Ile Ala		
225	230	235
Ser Val Val Lys Glu Leu Gly Ile Asp Gly Leu Ile Val Thr Asn Thr		240
245	250	255
Thr Val Ser Arg Pro Ala Gly Leu Gln Gly Ala Leu Arg Ser Glu Thr		
260	265	270
Gly Gly Leu Ser Gly Lys Pro Leu Arg Asp Leu Ser Thr Gln Thr Ile		
275	280	285

Arg Glu Met Tyr Ala Leu Thr Gln Gly Arg Val Pro Ile Ile Gly Val		
290	295	300
Gly Gly Val Ser Ser Gly Gln Asp Ala Leu Glu Lys Ile Arg Ala Gly		
305	310	315
Ala Ser Leu Val Gln Leu Tyr Thr Ala Leu Thr Phe Trp Gly Pro Pro		
325	330	335
Val Val Gly Lys Val Lys Arg Glu Leu Glu Ala Leu Leu Lys Glu Gln		
340	345	350
Gly Phe Gly Gly Val Thr Asp Ala Ile Gly Ala Asp His Arg Arg		
355	360	365

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<221> CDS
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<223> His26Ala DHODH mutant

<300>
<301> Davis et al.
<302> Histidine to Alanine mutants of Human Dihydroorotate
<303> Biochem. Pharmacol. (1997)
<304> 54
<306> 459-465

<400> 23
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Ala Thr Gly Asp Glu Arg Phe Tyr Ala Glu His Leu Met Pro Thr
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ctg cag ggg ctg ctg gac ccg gag tca gcc gcc aga ctg gct gtt cgc 96
Leu Gln Gly Leu Leu Asp Pro Glu Ser Ala Ala Arg Leu Ala Val Arg
20 25 30

ttc acc tcc ctg ggg ctc ctt cca cg ^g gcc aga ttt caa gac tct gac	144
Phe Thr Ser Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp	
35 40 45	
atg ctg gaa gtg aga gtt ctg ggc cat aaa ttc cga aat cca gta gga	192
Met Leu Glu Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly	
50 55 60	
att gct gca gga ttt gac aag cat ggg gaa gcc gtg gac gga ctt tat	240
Ile Ala Ala Gly Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr	
65 70 75	
aag atg ggc ttt ggt ttt gtt gag ata gga agt gtg act cca aaa cct	288
Lys Met Gly Phe Gly Phe Val Glu Ile Gly Ser Val Thr Pro Lys Pro	
80 85 90 95	
cag gaa gga aac cct aga ccc aga gtc ttc cgc ctc cct gag gac caa	336
Gln Glu Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln	
100 105 110	
gct gtc att aac agg tat gga ttt aac agt cac ggg ctt tca gtg gtg	384
Ala Val Ile Asn Arg Tyr Gly Phe Asn Ser His Gly Leu Ser Val Val	
115 120 125	
gaa cac agg tta cgg gcc aga cag cag aag cag gcc aag ctc aca gaa	432
Glu His Arg Leu Arg Ala Arg Gln Gln Lys Gln Ala Lys Leu Thr Glu	
130 135 140	
gat gga ctg cct ctg ggg gtc aac ttg ggg aag aac aag acc tca gtg	480
Asp Gly Leu Pro Leu Gly Val Asn Leu Gly Lys Asn Lys Thr Ser Val	
145 150 155	
gac gcc gcg gag gac tac gca gaa ggg gtg cgc gta ctg ggc ccc ctg	528
Asp Ala Ala Glu Asp Tyr Ala Glu Gly Val Arg Val Leu Gly Pro Leu	
160 165 170 175	
gcc gac tac ctg gtg aat gtg tcc agc ccc aac act gcc ggg ctg	576
Ala Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Ala Gly Leu	
180 185 190	
cgg agc ctt cag gga aag gcc gag ctg cgc cgc ctg ctg acc aag gtg	624
Arg Ser Leu Gln Gly Lys Ala Glu Leu Arg Arg Leu Leu Thr Lys Val	
195 200 205	
ctg cag gag agg gat ggc ttg cgg aga gtg cac agg ccg gca gtc ctg	672
Leu Gln Glu Arg Asp Gly Leu Arg Arg Val His Arg Pro Ala Val Leu	
210 215 220	
gtg aag atc gct cct gac ctc acc agc cag gat aag gag gac att gcc	720
Val Lys Ile Ala Pro Asp Leu Thr Ser Gln Asp Lys Glu Asp Ile Ala	
225 230 235	
agt gtg gtc aaa gag ttg ggc atc gat ggg ctg att gtt acg aac acc	768
Ser Val Val Lys Glu Leu Gly Ile Asp Gly Leu Ile Val Thr Asn Thr	
240 245 250 255	
acc gtg agt cgc cct gcg ggc ctc cag ggt gcc ctg cgc tct gaa aca	816
Thr Val Ser Arg Pro Ala Gly Leu Gln Gly Ala Leu Arg Ser Glu Thr	
260 265 270	
gga ggg ctg agt ggg aag ccc ctc cgg gat tta tca act caa acc att	864
Gly Gly Leu Ser Gly Lys Pro Leu Arg Asp Leu Ser Thr Gln Thr Ile	
275 280 285	
cgg gag atg tat gca ctc acc caa ggc cga gtt ccc ata att ggg gtt	912
Arg Glu Met Tyr Ala Leu Thr Gln Gly Arg Val Pro Ile Ile Gly Val	

290	295	300	
ggt ggt gtg agc agc ggg cag gac gcg ctg gag aag atc cg	gca ggg		960
Gly Gly Val Ser Ser Gly Gln Asp Ala Leu Glu Lys Ile Arg Ala Gly			
305	310	315	
gcc tcc ctg gtg cag ctg tac acg gcc ctc acc ttc tgg ggg cca ccc			1008
Ala Ser Leu Val Gln Leu Tyr Thr Ala Leu Thr Phe Trp Gly Pro Pro			
320	325	330	335
gtt gtg ggc aaa gtc aag cgg gaa ctg gag gcc ctt ctg aaa gag cag			1056
Val Val Gly Lys Val Lys Arg Glu Leu Glu Ala Leu Leu Lys Glu Gln			
340	345	350	
ggc ttt ggc gga gtc aca gat gcc att gga gca gat cat cg	agg		1101
Gly Phe Gly Gly Val Thr Asp Ala Ile Gly Ala Asp His Arg Arg			
355	360	365	

<210> 24
 <211> 366
 <212> PRT
 <213> Homo sapien

<400> 24

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Gln Gly Leu Leu Asp Pro Glu Ser Ala Ala Arg Leu Ala Val Arg Phe			
20	25	30	
Thr Ser Leu Gly Leu Leu Pro Arg Ala Arg Phe Gln Asp Ser Asp Met			
35	40	45	
Leu Glu Val Arg Val Leu Gly His Lys Phe Arg Asn Pro Val Gly Ile			
50	55	60	
Ala Ala Gly Phe Asp Lys His Gly Glu Ala Val Asp Gly Leu Tyr Lys			
65	70	75	80
Met Gly Phe Gly Phe Val Glu Ile Gly Ser Val Thr Pro Lys Pro Gln			
85	90	95	
Glu Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Glu Asp Gln Ala			
100	105	110	
Val Ile Asn Arg Tyr Gly Phe Asn Ser His Gly Leu Ser Val Val Glu			
115	120	125	
His Arg Leu Arg Ala Arg Gln Gln Lys Gln Ala Lys Leu Thr Glu Asp			
130	135	140	
Gly Leu Pro Leu Gly Val Asn Leu Gly Lys Asn Lys Thr Ser Val Asp			
145	150	155	160
Ala Ala Glu Asp Tyr Ala Glu Gly Val Arg Val Leu Gly Pro Leu Ala			
165	170	175	
Asp Tyr Leu Val Val Asn Val Ser Ser Pro Asn Thr Ala Gly Leu Arg			
180	185	190	
Ser Leu Gln Gly Lys Ala Glu Leu Arg Arg Leu Leu Thr Lys Val Leu			
195	200	205	
Gln Glu Arg Asp Gly Leu Arg Arg Val His Arg Pro Ala Val Leu Val			
210	215	220	
Lys Ile Ala Pro Asp Leu Thr Ser Gln Asp Lys Glu Asp Ile Ala Ser			
225	230	235	240
Val Val Lys Glu Leu Gly Ile Asp Gly Leu Ile Val Thr Asn Thr Thr			
245	250	255	
Val Ser Arg Pro Ala Gly Leu Gln Gly Ala Leu Arg Ser Glu Thr Gly			
260	265	270	
Gly Leu Ser Gly Lys Pro Leu Arg Asp Leu Ser Thr Gln Thr Ile Arg			
275	280	285	
Glu Met Tyr Ala Leu Thr Gln Gly Arg Val Pro Ile Ile Gly Val Gly			
290	295	300	
Gly Val Ser Ser Gly Gln Asp Ala Leu Glu Lys Ile Arg Ala Gly Ala			
305	310	315	320
Ser Leu Val Gln Leu Tyr Thr Ala Leu Thr Phe Trp Gly Pro Pro Val			
325	330	335	

Val Gly Lys Val Lys Arg Glu Leu Glu Ala Leu Leu Lys Glu Gln Gly
 340 345 350
 Phe Gly Gly Val Thr Asp Ala Ile Gly Ala Asp His Arg Arg
 355 360 365

<210> 25
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 <212> DNA
 <213> Aspergillus nidulans

<220>
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 <223> Aspergillus nidulans Val200Glu mutant DHODH cDNA

<221> mutation
 <222> 599
 <223> T to A mutatation

<400> 25

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Met	Ala	Thr	Asn	Ser	Phe	Arg	Lys	Leu	Thr	Phe	Ser	Gly	Ala	Ser	Arg	
1	5							10					15			

ctg	ggg	gtt	tgt	cgc	cgt	ctc	cca	cta	acc	tgc	aga	caa	ctt	cga	ttc	96
Leu	Gly	Gly	Cys	Arg	Arg	Leu	Pro	Leu	Thr	Cys	Arg	Gln	Leu	Arg	Phe	
				20				25					30			

gcc	tcc	gac	agc	gga	gcc	gca	gcf	gca	act	aca	aaa	gca	acg	gcc	gaa	144
Ala	Ser	Asp	Ser	Gly	Ala	Ala	Ala	Ala	Thr	Thr	Lys	Ala	Thr	Ala	Glu	
				35				40					45			

tca	gca	gcc	gag	tca	gct	agt	ata	aac	gtc	aaa	gag	gca	ccc	aaa	aag	192
Ser	Ala	Ala	Glu	Ser	Ala	Ser	Ile	Asn	Val	Lys	Glu	Ala	Pro	Lys	Lys	
				50			55					60				

gcc	gga	cg	ggc	ctg	cg	cg	ac	gt	ctg	gga	ac	tc	tt	g	ctg	240
Ala	Gly	Arg	Gly	Leu	Arg	Arg	Thr	Val	Leu	Gly	Thr	Ser	Leu	Ala	Leu	
				65			70					75			80	

ac	ctg	ctg	gtt	gga	ta	gt	tc	ta	gg	ac	g	ac	cc	g	ag	gt	288
Thr	Leu	Leu	Val	Gly	Tyr	Val	Tyr	Gly	Thr	Asp	Thr	Arg	Ala	Ser	Val		
				85			90					95					

cat	cg	ta	gg	gtt	gt	cc	ctg	at	ag	gca	tt	ta	cct	gt	gc	336
His	Arg	Tyr	Gly	Val	Val	Pro	Leu	Ile	Arg	Ala	Leu	Tyr	Pro	Asp	Ala	
				100				105				110				

gaa	gat	gc	cat	cat	att	gg	gt	at	ct	ta	aag	at	ct	ta	aag	384
Glu	Asp	Ala	His	His	Ile	Gly	Val	Asp	Thr	Leu	Lys	Met	Leu	Tyr	Lys	
					115			120				125				

ta	gg	ct	ca	ag	gaa	cg	gg	gat	cc	gat	gga	gat	gg	g	cg	432
Tyr	Gly	Leu	His	Pro	Arg	Glu	Arg	Gly	Asp	Pro	Asp	Gly	Asp	Gly	Ala	
					130			135			140					

ctg	gc	ac	ga	gt	tt	gg	ta	ac	ct	ta	ac	cc	at	gg	at	480
Leu	Ala	Thr	Glu	Val	Phe	Gly	Tyr	Thr	Leu	Ser	Asn	Pro	Ile	Gly	Ile	
					145			150			155		160			

tc	gg	gc	ct	ga	aa	gt	ga	at	c	ct	gt	tc	gg	ct	528
Ser	Gly	Leu	Asp	Lys	His	Ala	Glu	Ile	Pro	Asp	Pro	Leu	Phe	Ala	
					165			170			175				

at	gg	c	cc	at	gt	ga	at	c	ct	gt	tc	gg	cc	tt	cc	ca	576
Ile	Gly	Pro	Ala	Ile	Val	Glu	Val	Gly	Gly	Thr	Thr	Pro	Leu	Pro	Gln		
					180			185			190						

gat ggt aac ccg cgt cct cgc gaa ttc cga ctt cca tca cag aga gcg	624
Asp Gly Asn Pro Arg Pro Arg Glu Phe Arg Leu Pro Ser Gln Arg Ala	
195 200 205	
atg ata aac cgg tac ggc ctc aac tcc aaa ggc gca gat cac atg gca	672
Met Ile Asn Arg Tyr Gly Leu Asn Ser Lys Gly Ala Asp His Met Ala	
210 215 220	
gct atc ttg gag caa cga gta cgc gat ttt gcc tac gca aac gga ttt	720
Ala Ile Leu Glu Gln Arg Val Arg Asp Phe Ala Tyr Ala Asn Gly Phe	
225 230 235 240	
ggg gca tac gat gcg gct aag cag cgt gta ttg gac ggc gaa gct ggt	768
Gly Ala Tyr Asp Ala Ala Lys Gln Arg Val Leu Asp Gly Glu Ala Gly	
245 250 255	
gtg cca cca ggt agt ctt cag cct ggt aag ctt tta gct gtc caa gtg	816
Val Pro Pro Gly Ser Leu Gln Pro Gly Lys Leu Leu Ala Val Gln Val	
260 265 270	
gca aag aac aag gcc act cct gac ggc gac att gaa gcc atc aag cgc	864
Ala Lys Asn Lys Ala Thr Pro Asp Gly Asp Ile Glu Ala Ile Lys Arg	
275 280 285	
gac tat gtg tat tgc gtg gac cgt gtg gcc aaa tac gct gat att ctt	912
Asp Tyr Val Tyr Cys Val Asp Arg Val Ala Lys Tyr Ala Asp Ile Leu	
290 295 300	
gtt gtg aat gta tcg agc ccc aac aca ccc ggt ctc cgt gac ctt caa	960
Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly Leu Arg Asp Leu Gln	
305 310 315 320	
gcc act gcc ccg ctc aca gct atc ttg agt gct gtc gtt ggc gcg gca	1008
Ala Thr Ala Pro Leu Thr Ala Ile Leu Ser Ala Val Val Gly Ala Ala	
325 330 335	
aag agc gtg aac cgc aag acc aaa cca tat gtt atg gtc aag gtc agt	1056
Lys Ser Val Asn Arg Lys Thr Lys Pro Tyr Val Met Val Lys Val Ser	
340 345 350	
ccg gat gaa gac tca gat gaa caa gtc tct ggt atc tgc gac gcc gtc	1104
Pro Asp Glu Asp Ser Asp Glu Gln Val Ser Gly Ile Cys Asp Ala Val	
355 360 365	
cga gca tcc ggt gtc gac gga gtg att gtc gga aac aca aca aac cgt	1152
Arg Ala Ser Gly Val Asp Gly Val Ile Val Gly Asn Thr Thr Asn Arg	
370 375 380	
cgc ccc gac cct ata ccc caa ggt tac act ctt ccg gcc aag gag cag	1200
Arg Pro Asp Pro Ile Pro Gln Gly Tyr Thr Leu Pro Ala Lys Glu Gln	
385 390 395 400	
gca acg ttg aaa gaa acc ggc ggg tat tca ggt cca cag ctg ttc gat	1248
Ala Thr Leu Lys Glu Thr Gly Tyr Ser Gly Pro Gln Leu Phe Asp	
405 410 415	
cgc aca gtg gcc ctt gtg gct cgg tac cgc tcc atg ctg gat gcg gag	1296
Arg Thr Val Ala Leu Val Ala Arg Tyr Arg Ser Met Leu Asp Ala Glu	
420 425 430	
tcg gaa acg gcc gga tcc gcc aag gat tca gca gcg acc ata gcg caa	1344
Ser Glu Thr Ala Gly Ser Ala Lys Asp Ser Ala Ala Thr Ile Ala Gln	
435 440 445	
aca gag cca ggc tcg gaa aac gtt cct cct gtg gaa gcg cca agc gga	1392
Thr Glu Pro Gly Ser Glu Asn Val Pro Pro Val Glu Ala Pro Ser Gly	

450

455

460

ctg	ccg	cgc	aaa	gtt	atc	ttc	gct	tcg	ggt	ggt	atc	acc	aac	ggg	aag	1440
Leu	Pro	Arg	Lys	Val	Ile	Phe	Ala	Ser	Gly	Gly	Ile	Thr	Asn	Gly	Lys	
465				470					475				480			
cag	gct	cac	gct	gtt	tta	gac	aca	ggg	gca	tct	gtt	gcc	atg	atg	tac	1488
Gln	Ala	His	Ala	Val	Leu	Asp	Thr	Gly	Ala	Ser	Val	Ala	Met	Met	Tyr	
				485					490				495			
acc	ggt	gtg	gtc	tat	ggt	ggc	gtc	ggc	act	gtc	act	cga	gtg	aag	caa	1536
Thr	Gly	Val	Val	Tyr	Gly	Gly	Val	Gly	Thr	Val	Thr	Arg	Val	Lys	Gln	
			500				505					510				
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Glu	Leu	Arg	Thr	Ala	Lys	Lys	Glu									
	515				520											

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<211> 520

<212> PRT

<213> Aspergillus nidulans

<400> 26

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						20			25				30			
Ala	Ser	Asp	Ser	Gly	Ala	Ala	Ala	Ala	Thr	Thr	Lys	Ala	Thr	Ala	Glu	
						35			40				45			
Ser	Ala	Ala	Glu	Ser	Ala	Ser	Ile	Asn	Val	Lys	Glu	Ala	Pro	Lys	Lys	
						50			55				60			
Ala	Gly	Arg	Gly	Leu	Arg	Arg	Thr	Val	Leu	Gly	Thr	Ser	Leu	Ala	Leu	
					65			70			75			80		
Thr	Leu	Leu	Val	Gly	Tyr	Val	Tyr	Gly	Thr	Asp	Thr	Arg	Ala	Ser	Val	
						85			90				95			
His	Arg	Tyr	Gly	Val	Val	Pro	Leu	Ile	Arg	Ala	Leu	Tyr	Pro	Asp	Ala	
						100			105				110			
Glu	Asp	Ala	His	His	Ile	Gly	Val	Asp	Thr	Leu	Lys	Met	Leu	Tyr	Lys	
						115			120				125			
Tyr	Gly	Leu	His	Pro	Arg	Glu	Arg	Gly	Asp	Pro	Asp	Gly	Asp	Gly	Ala	
					130			135				140				
Leu	Ala	Thr	Glu	Val	Phe	Gly	Tyr	Thr	Leu	Ser	Asn	Pro	Ile	Gly	Ile	
					145			150			155			160		
Ser	Gly	Gly	Leu	Asp	Lys	His	Ala	Glu	Ile	Pro	Asp	Pro	Leu	Phe	Ala	
						165			170				175			
Ile	Gly	Pro	Ala	Ile	Val	Glu	Val	Gly	Gly	Thr	Thr	Pro	Leu	Pro	Gln	
						180			185				190			
Asp	Gly	Asn	Pro	Arg	Pro	Arg	Glu	Phe	Arg	Leu	Pro	Ser	Gln	Arg	Ala	
						195			200				205			
Met	Ile	Asn	Arg	Tyr	Gly	Leu	Asn	Ser	Lys	Gly	Ala	Asp	His	Met	Ala	
						210			215				220			
Ala	Ile	Leu	Glu	Gln	Arg	Val	Arg	Asp	Phe	Ala	Tyr	Ala	Asn	Gly	Phe	
						225			230				235			240
Gly	Ala	Tyr	Asp	Ala	Ala	Lys	Gln	Arg	Val	Leu	Asp	Gly	Glu	Ala	Gly	
						245			250				255			
Val	Pro	Pro	Gly	Ser	Leu	Gln	Pro	Gly	Lys	Leu	Leu	Ala	Val	Gln	Val	
						260			265				270			
Ala	Lys	Asn	Lys	Ala	Thr	Pro	Asp	Gly	Asp	Ile	Glu	Ala	Ile	Lys	Arg	
						275			280				285			
Asp	Tyr	Val	Tyr	Cys	Val	Asp	Arg	Val	Ala	Lys	Tyr	Ala	Asp	Ile	Leu	
						290			295				300			
Val	Val	Asn	Val	Ser	Ser	Pro	Asn	Thr	Pro	Gly	Leu	Arg	Asp	Leu	Gln	
						305			310				315			320
Ala	Thr	Ala	Pro	Leu	Thr	Ala	Ile	Leu	Ser	Ala	Val	Val	Gly	Ala	Ala	
						325						330			335	

Lys	Ser	Val	Asn	Arg	Lys	Thr	Lys	Pro	Tyr	Val	Met	Val	Lys	Val	Ser
340							345						350		
Pro	Asp	Glu	Asp	Ser	Asp	Glu	Gln	Val	Ser	Gly	Ile	Cys	Asp	Ala	Val
355							360					365			
Arg	Ala	Ser	Gly	Val	Asp	Gly	Val	Ile	Val	Gly	Asn	Thr	Thr	Asn	Arg
370							375					380			
Arg	Pro	Asp	Pro	Ile	Pro	Gln	Gly	Tyr	Thr	Leu	Pro	Ala	Lys	Glu	Gln
385							390					395			400
Ala	Thr	Leu	Lys	Glu	Thr	Gly	Gly	Tyr	Ser	Gly	Pro	Gln	Leu	Phe	Asp
													415		
Arg	Thr	Val	Ala	Leu	Val	Ala	Arg	Tyr	Arg	Ser	Met	Leu	Asp	Ala	Glu
													420		
Ser	Glu	Thr	Ala	Gly	Ser	Ala	Lys	Asp	Ser	Ala	Ala	Thr	Ile	Ala	Gln
													435		
Thr	Glu	Pro	Gly	Ser	Glu	Asn	Val	Pro	Pro	Val	Glu	Ala	Pro	Ser	Gly
													450		
Leu	Pro	Arg	Lys	Val	Ile	Phe	Ala	Ser	Gly	Gly	Ile	Thr	Asn	Gly	Lys
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Gln	Ala	His	Ala	Val	Leu	Asp	Thr	Gly	Ala	Ser	Val	Ala	Met	Met	Tyr
													485		
Thr	Gly	Val	Val	Tyr	Gly	Gly	Val	Gly	Thr	Val	Thr	Arg	Val	Lys	Gln
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Glu	Leu	Arg	Thr	Ala	Lys	Lys	Glu								
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<210> 27
<211> 1560
<212> DNA
<213> Aspergillus nidulans

<220>
<221> CDS
<222> (1) ... (1560)
<223> Aspergillus nidulans Alal15Val mutant DHODH cDNA

<221> mutation
<222> 344
<223> C to T mutation

<400> 27

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Met	Ala	Thr	Asn	Ser	Phe	Arg	Lys	Leu	Thr	Phe	Ser	Gly	Ala	Ser	Arg		
1															15		
ctg	ggt	ggt	tgt	cgc	cgt	ctc	cca	cta	acc	tgc	aga	caa	ctt	cga	ttc	96	
Leu	Gly	Gly	Cys	Arg	Arg	Leu	Pro	Leu	Thr	Cys	Arg	Gln	Leu	Arg	Phe		
															30		
gcc	tcc	gac	agc	gga	gcc	gca	gcg	gca	act	aca	aaa	gca	acg	gcc	gaa	144	
Ala	Ser	Asp	Ser	Gly	Ala	Ala	Ala	Ala	Ala	Thr	Thr	Lys	Ala	Thr	Ala	Glu	
															35		
															40		
tca	gca	gcc	gag	tca	gct	agt	ata	aac	gtc	aaa	gag	gca	ccc	aaa	aag	192	
Ser	Ala	Ala	Glu	Ser	Ala	Ser	Ile	Asn	Val	Lys	Glu	Ala	Pro	Lys	Lys		
															50		
															55		
gcc	gga	cg	gg	ct	cg	cg	ac	gt	ct	gg	ac	tc	tg	gc	ct	240	
Ala	Gly	Arg	Gly	Leu	Arg	Arg	Thr	Val	Leu	Gly	Thr	Ser	Leu	Ala	Leu		
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															70		
ac	ct	ct	gt	gg	ta	gt	ta	gg	ac	ga	ac	cg	gc	ag	gt	288	
Thr	Leu	Leu	Val	Gly	Tyr	Val	Tyr	Gly	Thr	Asp	Thr	Arg	Ala	Ser	Val		
															85		
															90		
cat	cg	ta	gg	gt	gt	cc	ct	at	ag	ga	tt	ta	c	ga	gc	336	
His	Arg	Tyr	Gly	Val	Val	Pro	Leu	Ile	Arg	Ala	Leu	Tyr	Pro	Asp	Ala		
															100		
															105		
															110		

gaa gat gtg cat cat att ggt gtc gat act tta aag atg ctg tat aag	384
Glu Asp Val His His Ile Gly Val Asp Thr Leu Lys Met Leu Tyr Lys	
115 120 125	
tat ggt ctg cat cca agg gaa cggt ggg gat ccg gat gga gat ggg gcg	432
Tyr Gly Leu His Pro Arg Glu Arg Gly Asp Pro Asp Gly Asp Gly Ala	
130 135 140	
ctg gcg aca gag gtc ttt ggg tat aca ctg tca aac cca att ggc ata	480
Leu Ala Thr Glu Val Phe Gly Tyr Thr Leu Ser Asn Pro Ile Gly Ile	
145 150 155 160	
tcg ggc ggc ctg gac aag cat gct gag atc cct gat ccg ctg ttc gcg	528
Ser Gly Gly Leu Asp Lys His Ala Glu Ile Pro Asp Pro Leu Phe Ala	
165 170 175	
atc ggt cct gcc att gtc gaa gtc ggg ggt acg aca ccc tta cca cag	576
Ile Gly Pro Ala Ile Val Glu Val Gly Gly Thr Thr Pro Leu Pro Gln	
180 185 190	
gat ggt aac ccg cgt cct cgc gta ttc cga ctt cca tca cag aga gcg	624
Asp Gly Asn Pro Arg Pro Arg Val Phe Arg Leu Pro Ser Gln Arg Ala	
195 200 205	
atg ata aac cgg tac ggc ctc aac tcc aaa ggc gca gat cac atg gca	672
Met Ile Asn Arg Tyr Gly Leu Asn Ser Lys Gly Ala Asp His Met Ala	
210 215 220	
gct atc ttg gag caa cga gta cgc gat ttt gcc tac gca aac gga ttt	720
Ala Ile Leu Glu Gln Arg Val Arg Asp Phe Ala Tyr Ala Asn Gly Phe	
225 230 235 240	
ggg gca tac gat gcg gct aag cag cgt gta ttg gac ggc gaa gct ggt	768
Gly Ala Tyr Asp Ala Ala Lys Gln Arg Val Leu Asp Gly Glu Ala Gly	
245 250 255	
gtg cca cca ggt agt ctt cag cct ggt aag ctt tta gct gtc caa gtg	816
Val Pro Pro Gly Ser Leu Gln Pro Gly Lys Leu Leu Ala Val Gln Val	
260 265 270	
gca aag aac aag gcc act cct gac ggc gac att gaa gcc atc aag cgc	864
Ala Lys Asn Lys Ala Thr Pro Asp Gly Asp Ile Glu Ala Ile Lys Arg	
275 280 285	
gac tat gtg tat tgc gtg gac cgt gtg gcc aaa tac gct gat att ctt	912
Asp Tyr Val Tyr Cys Val Asp Arg Val Ala Lys Tyr Ala Asp Ile Leu	
290 295 300	
gtt gtg aat gta tcg agc ccc aac aca ccc ggt ctc cgt gac ctt caa	960
Val Val Asn Val Ser Ser Pro Asn Thr Pro Gly Leu Arg Asp Leu Gln	
305 310 315 320	
gcc act gcc ccg ctc aca gct atc ttg agt gct gtc gtt ggc gcg gca	1008
Ala Thr Ala Pro Leu Thr Ala Ile Leu Ser Ala Val Val Gly Ala Ala	
325 330 335	
aag agc gtg aac cgc aag acc aaa cca tat gtt atg gtc aag gtc agt	1056
Lys Ser Val Asn Arg Lys Thr Lys Pro Tyr Val Met Val Lys Val Ser	
340 345 350	
ccg gat gaa gac tca gat gaa caa gtc tct ggt atc tgc gac gcc gtc	1104
Pro Asp Glu Asp Ser Asp Glu Gln Val Ser Gly Ile Cys Asp Ala Val	
355 360 365	
cga gca tcc ggt gtc gac gga gtg att gtc gga aac aca aca aac cgt	1152
Arg Ala Ser Gly Val Asp Gly Val Ile Val Gly Asn Thr Thr Asn Arg	

370	375	380	
cgc ccc gac cct ata ccc caa ggt tac act ctt ccg gcc aag gag cag			1200
Arg Pro Asp Pro Ile Pro Gln Gly Tyr Thr Leu Pro Ala Lys Glu Gln			
385	390	395	400
gca acg ttg aaa gaa acc ggc ggg tat tca ggt cca cag ctg ttc gat			1248
Ala Thr Leu Lys Glu Thr Gly Gly Tyr Ser Gly Pro Gln Leu Phe Asp			
405	410	415	
cgc aca gtg gcc ctt gtg gct cgg tac cgc tcc atg ctg gat gcg gag			1296
Arg Thr Val Ala Leu Val Ala Arg Tyr Arg Ser Met Leu Asp Ala Glu			
420	425	430	
tcg gaa acg gcc gga tcc gcc aag gat tca gca gcg acc ata gcg caa			1344
Ser Glu Thr Ala Gly Ser Ala Lys Asp Ser Ala Ala Thr Ile Ala Gln			
435	440	445	
aca gag cca ggc tcg gaa aac gtt cct cct gtg gaa gcg cca agc gga			1392
Thr Glu Pro Gly Ser Glu Asn Val Pro Pro Val Glu Ala Pro Ser Gly			
450	455	460	
ctg ccg cgc aaa gtt atc ttc gct tcg ggt ggt atc acc aac ggg aag			1440
Leu Pro Arg Lys Val Ile Phe Ala Ser Gly Gly Ile Thr Asn Gly Iys			
465	470	475	480
cag gct cac gct gtt tta gac aca ggg gca tct gtt gcc atg atg tac			1488
Gln Ala His Ala Val Leu Asp Thr Gly Ala Ser Val Ala Met Met Tyr			
485	490	495	
acc ggt gtg gtc tat ggt ggc gtc ggc act gtc act cga gtg aag caa			1536
Thr Gly Val Val Tyr Gly Gly Val Gly Thr Val Thr Arg Val Lys Gln			
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gaa ctt cga acg gcg aaa aag gag			1560
Glu Leu Arg Thr Ala Lys Lys Glu			
515	520		

<210> 28

<211> 520

<212> PRT

<213> Aspergillus nidulans

<400> 28

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Ala Ser Asp Ser Gly Ala Ala Ala Thr Thr Lys Ala Thr Ala Glu			
35	40	45	
Ser Ala Ala Glu Ser Ala Ser Ile Asn Val Lys Glu Ala Pro Lys Lys			
50	55	60	
Ala Gly Arg Gly Leu Arg Arg Thr Val Leu Gly Thr Ser Leu Ala Leu			
65	70	75	80
Thr Leu Leu Val Gly Tyr Val Tyr Gly Thr Asp Thr Arg Ala Ser Val			
85	90	95	
His Arg Tyr Gly Val Val Pro Leu Ile Arg Ala Leu Tyr Pro Asp Ala			
100	105	110	
Glu Asp Val His His Ile Gly Val Asp Thr Leu Lys Met Leu Tyr Lys			
115	120	125	
Tyr Gly Leu His Pro Arg Glu Arg Gly Asp Pro Asp Gly Asp Gly Ala			
130	135	140	
Leu Ala Thr Glu Val Phe Gly Tyr Thr Leu Ser Asn Pro Ile Gly Ile			
145	150	155	160
Ser Gly Gly Leu Asp Lys His Ala Glu Ile Pro Asp Pro Leu Phe Ala			
165	170	175	

Ile	Gly	Pro	Ala	Ile	Val	Glu	Val	Gly	Gly	Thr	Thr	Pro	Leu	Pro	Gln
				180				185						190	
Asp	Gly	Asn	Pro	Arg	Pro	Arg	Val	Phe	Arg	Leu	Pro	Ser	Gln	Arg	Ala
				195			200					205			
Met	Ile	Asn	Arg	Tyr	Gly	Leu	Asn	Ser	Lys	Gly	Ala	Asp	His	Met	Ala
				210			215				220				
Ala	Ile	Leu	Glu	Gln	Arg	Val	Arg	Asp	Phe	Ala	Tyr	Ala	Asn	Gly	Phe
				225			230			235			240		
Gly	Ala	Tyr	Asp	Ala	Ala	Lys	Gln	Arg	Val	Leu	Asp	Gly	Glu	Ala	Gly
				245			250				255				
Val	Pro	Pro	Gly	Ser	Leu	Gln	Pro	Gly	Lys	Leu	Leu	Ala	Val	Gln	Val
				260			265				270				
Ala	Lys	Asn	Lys	Ala	Thr	Pro	Asp	Gly	Asp	Ile	Glu	Ala	Ile	Lys	Arg
				275			280				285				
Asp	Tyr	Val	Tyr	Cys	Val	Asp	Arg	Val	Ala	Lys	Tyr	Ala	Asp	Ile	Leu
				290			295				300				
Val	Val	Asn	Val	Ser	Ser	Pro	Asn	Thr	Pro	Gly	Leu	Arg	Asp	Leu	Gln
				305			310			315			320		
Ala	Thr	Ala	Pro	Leu	Thr	Ala	Ile	Leu	Ser	Ala	Val	Val	Gly	Ala	Ala
				325			330				335				
Lys	Ser	Val	Asn	Arg	Lys	Thr	Lys	Pro	Tyr	Val	Met	Val	Lys	Val	Ser
				340			345			350			350		
Pro	Asp	Glu	Asp	Ser	Asp	Glu	Gln	Val	Ser	Gly	Ile	Cys	Asp	Ala	Val
				355			360			365					
Arg	Ala	Ser	Gly	Val	Asp	Gly	Val	Ile	Val	Gly	Asn	Thr	Thr	Asn	Arg
				370			375			380					
Arg	Pro	Asp	Pro	Ile	Pro	Gln	Gly	Tyr	Thr	Leu	Pro	Ala	Lys	Glu	Gln
				385			390			395			400		
Ala	Thr	Leu	Lys	Glu	Thr	Gly	Gly	Tyr	Ser	Gly	Pro	Gln	Leu	Phe	Asp
				405			410				415				
Arg	Thr	Val	Ala	Leu	Val	Ala	Arg	Tyr	Arg	Ser	Met	Leu	Asp	Ala	Glu
				420			425				430				
Ser	Glu	Thr	Ala	Gly	Ser	Ala	Lys	Asp	Ser	Ala	Ala	Thr	Ile	Ala	Gln
				435			440				445				
Thr	Glu	Pro	Gly	Ser	Glu	Asn	Val	Pro	Pro	Val	Glu	Ala	Pro	Ser	Gly
				450			455			460					
Leu	Pro	Arg	Lys	Val	Ile	Phe	Ala	Ser	Gly	Gly	Ile	Thr	Asn	Gly	Lys
				465			470			475			480		
Gln	Ala	His	Ala	Val	Leu	Asp	Thr	Gly	Ala	Ser	Val	Ala	Met	Met	Tyr
				485			490				495				
Thr	Gly	Val	Val	Tyr	Gly	Gly	Val	Gly	Thr	Val	Thr	Arg	Val	Lys	Gln
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Glu	Leu	Arg	Thr	Ala	Lys	Lys	Glu								
				515			520								

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<211> 1707

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (67) . . . (1611)

<223> wild-type IMP dehyrdogenase cDNA

<400> 29

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Met	Ala	Asp	Tyr	Leu	Ile	Ser	Gly	Gly	Thr	Ser	Tyr	Val	Pro		
1				5					10						

gac	gac	ggg	ctc	aca	gca	cag	cag	ctc	ttc	aac	tgc	ggg	gac	ggc	ctc
Asp	Asp	Gly	Leu	Thr	Ala	Gln	Gln	Leu	Phe	Asn	Cys	Gly	Asp	Gly	Leu
15				20					25				30		

acc	tac	aat	gat	ttt	ctc	att	ctt	cct	ggg	tat	atc	gac	ttc	act	gca
Thr	Tyr	Asn	Asp	Phe	Leu	Ile	Leu	Pro	Gly	Tyr	Ile	Asp	Phe	Thr	Ala
														204	

35	40	45	
gat cag gtg gac ttg acg tct gct cta act aag aag att aca cta aag Asp Gln Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys 50	55	60	252
acc cca ttg gtt tcc tca ccc atg gac act gtc aca gag gct gga atg Thr Pro Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met 65	70	75	300
gcc atc gcg atg gcg ctt aca gga ggt att ggt ttc atc cac cac aac Ala Ile Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn 80	85	90	348
tgc aca cct gaa ttc cag gcc aat gaa gtt cg ^g aaa gtg aag aaa tac Cys Thr Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr 95	100	105	396
gaa cag gga ttc atc act gac ccc gtg gtc ctt agc ccc aag gat cgt Glu Gln Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg 115	120	125	444
gta cgc gat gtt ttt gag gcc aaa gcc agg cat ggc ttc tgt ggt atc Val Arg Asp Val Phe Glu Ala Lys Ala Arg His Gly Phe cys Gly Ile 130	135	140	492
ccc atc aca gat aca ggc cgg atg ggg agt cga ttg gtg ggc atc atc Pro Ile Thr Asp Thr Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile 145	150	155	540
tcc tca agg gac att gat ttc ctc aag gag gaa gag cat gac cgg ttc Ser Ser Arg Asp Ile Asp Phe Leu Lys Glu Glu His Asp Arg Phe 160	165	170	588
ttg gaa gag atc atg act aag agg gaa gat ttg gtg gtc gcc cct gcc Leu Glu Glu Ile Met Thr Lys Arg Glu Asp Leu Val Val Ala Pro Ala 175	180	185	636
ggc gtc act ctg aaa gag gca aat gag att ctg cag cga agt aaa aag Gly Val Thr Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys 195	200	205	684
gga aag ttg ccc att gtg aat gaa aat gat gag ctg gta gcc atc att Gly Lys Leu Pro Ile Val Asn Glu Asn Asp Glu Leu Val Ala Ile Ile 210	215	220	732
gcc cg ^g aca gac cta aag aat cgt gat tac ccc ctg gcc tcc aaa Ala Arg Thr Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys 225	230	235	780
gat gcc aag aag caa ctg ctg tgt ggg gca gcc att ggc act cat gag Asp Ala Lys Lys Gln Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu 240	245	250	828
gat gac aag tat agg ctg gac tta ctg gcc ctt gct ggt gtg gat gta Asp Asp Lys Tyr Arg Leu Asp Leu Ala Leu Ala Gly Val Asp Val 255	260	265	876
gtg gtt ttg gac tct tcc cag gga aac tcc atc ttc caa atc aat atg Val Val Leu Asp Ser Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met 275	280	285	924
atc aaa tac atc aag gag aag tat ccc agt cta cag gtc att gga ggc Ile Lys Tyr Ile Lys Glu Lys Tyr Pro Ser Leu Gln Val Ile Gly Gly 290	295	300	972
aat gta gtc act gct gcg caa gcc aag aac ctc ata gat gca ggt gta			1020

Asn Val Val Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val
 305 310 315

gat gct ttg cga gtc ggc atg gga agt ggt tcc atc tgc atc acc cag 1068
 Asp Ala Leu Arg Val Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln
 320 325 330

gaa gtg ttg gcc tgt ggg cgg ccc caa gcc aca gca gtg tac aag gtc 1116
 Glu Val Leu Ala Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val
 335 340 345 350

tct gag tat gcc cgt cgc ttt ggt gtt cct gtt att gct gat gga gga 1164
 Ser Glu Tyr Ala Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly
 355 360 365

atc caa aat gtg ggt cat att gcc aaa gct ttg gct ctt ggg gct tcc 1212
 Ile Gln Asn Val Gly His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser
 370 375 380

aca gtc atg atg ggc tcc ctc ctg gct gcc acc act gag gcc cct ggc 1260
 Thr Val Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly
 385 390 395

gag tac ttc ttc tca gat ggg atc cgg ctg aag aaa tac cga ggt atg 1308
 Glu Tyr Phe Phe Ser Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met
 400 405 410

ggt tct ctt gat gcc atg gac aaa cat ctc agc agc cag aac cga tac 1356
 Gly Ser Leu Asp Ala Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr
 415 420 425 430

ttc agt gaa gct gac aaa atc aaa gtg gcc caa gga gtt tca ggg gca 1404
 Phe Ser Glu Ala Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala
 435 440 445

gtg cag gac aag ggg tct atc cac aag ttc gtt cct tac ctg att gct 1452
 Val Gln Asp Lys Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala
 450 455 460

ggc atc cag cat tcc tgt caa gac att ggt gcc aag agt tta acc caa 1500
 Gly Ile Gln His Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln
 465 470 475

gtc aga gcc atg acg tac tcg ggg gag ctt aaa ttt gag aag agg aca 1548
 Val Arg Ala Met Thr Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr
 480 485 490

tcc tct gct cag gtg gaa ggt ggc gtc cac agc ctc cat tcg tac gag 1596
 Ser Ser Ala Gln Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu
 495 500 505 510

aaa cgg ctt ttc tga aaacagatcc agtatatgcc ttgaattttt caataaaaagt 1651
 Lys Arg Leu Phe *

ttggaaaaaa aaaagtgaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaa 1707

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 <211> 514
 <212> PRT
 <213> Mus musculus

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35						40						45			
Val	Asp	Leu	Thr	Ser	Ala	Leu	Thr	Lys	Lys	Ile	Thr	Leu	Lys	Thr	Pro
50						55					60				
Leu	Val	Ser	Ser	Pro	Met	Asp	Thr	Val	Thr	Glu	Ala	Gly	Met	Ala	Ile
65					70				75				80		
Ala	Met	Ala	Leu	Thr	Gly	Gly	Ile	Gly	Phe	Ile	His	His	Asn	Cys	Thr
					85			90					95		
Pro	Glu	Phe	Gln	Ala	Asn	Glu	Val	Arg	Lys	Val	Lys	Lys	Tyr	Glu	Gln
			100				105					110			
Gly	Phe	Ile	Thr	Asp	Pro	Val	Val	Leu	Ser	Pro	Lys	Asp	Arg	Val	Arg
		115				120					125				
Asp	Val	Phe	Glu	Ala	Lys	Ala	Arg	His	Gly	Phe	Cys	Gly	Ile	Pro	Ile
	130				135				140						
Thr	Asp	Thr	Gly	Arg	Met	Gly	Ser	Arg	Leu	Val	Gly	Ile	Ile	Ser	Ser
145				150				155				160			
Arg	Asp	Ile	Asp	Phe	Leu	Lys	Glu	Glu	Glu	His	Asp	Arg	Phe	Leu	Glu
		165				170			175						
Glu	Ile	Met	Thr	Lys	Arg	Glu	Asp	Leu	Val	Val	Ala	Pro	Ala	Gly	Val
		180				185				190					
Thr	Leu	Lys	Glu	Ala	Asn	Glu	Ile	Leu	Gln	Arg	Ser	Lys	Lys	Gly	Lys
		195				200				205					
Leu	Pro	Ile	Val	Asn	Glu	Asn	Asp	Glu	Leu	Val	Ala	Ile	Ile	Ala	Arg
	210			215				220							
Thr	Asp	Leu	Lys	Lys	Asn	Arg	Asp	Tyr	Pro	Leu	Ala	Ser	Lys	Asp	Ala
225				230					235				240		
Lys	Lys	Gln	Leu	Leu	Cys	Gly	Ala	Ala	Ile	Gly	Thr	His	Glu	Asp	Asp
			245				250					255			
Lys	Tyr	Arg	Leu	Asp	Leu	Leu	Ala	Leu	Ala	Gly	Val	Asp	Val	Val	Val
		260				265			270						
Leu	Asp	Ser	Ser	Gln	Gly	Asn	Ser	Ile	Phe	Gln	Ile	Asn	Met	Ile	Lys
		275				280				285					
Tyr	Ile	Lys	Glu	Lys	Tyr	Pro	Ser	Leu	Gln	Val	Ile	Gly	Gly	Asn	Val
	290				295				300						
Val	Thr	Ala	Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	Asp	Ala
305				310					315				320		
Leu	Arg	Val	Gly	Met	Gly	Ser	Gly	Ser	Ile	Cys	Ile	Thr	Gln	Glu	Val
		325					330				335				
Leu	Ala	Cys	Gly	Arg	Pro	Gln	Ala	Thr	Ala	Val	Tyr	Lys	Val	Ser	Glu
		340				345				350					
Tyr	Ala	Arg	Arg	Phe	Gly	Val	Pro	Val	Ile	Ala	Asp	Gly	Gly	Ile	Gln
		355				360				365					
Asn	Val	Gly	His	Ile	Ala	Lys	Ala	Leu	Ala	Leu	Gly	Ala	Ser	Thr	Val
	370				375				380						
Met	Met	Gly	Ser	Leu	Leu	Ala	Ala	Thr	Thr	Glu	Ala	Pro	Gly	Glu	Tyr
385				390					395				400		
Phe	Phe	Ser	Asp	Gly	Ile	Arg	Leu	Lys	Lys	Tyr	Arg	Gly	Met	Gly	Ser
			405				410				415				
Leu	Asp	Ala	Met	Asp	Lys	His	Leu	Ser	Ser	Gln	Asn	Arg	Tyr	Phe	Ser
			420				425				430				
Glu	Ala	Asp	Lys	Ile	Lys	Val	Ala	Gln	Gly	Val	Ser	Gly	Ala	Val	Gln
			435			440				445					
Asp	Lys	Gly	Ser	Ile	His	Lys	Phe	Val	Pro	Tyr	Leu	Ile	Ala	Gly	Ile
	450				455			460							
Gln	His	Ser	Cys	Gln	Asp	Ile	Gly	Ala	Lys	Ser	Leu	Thr	Gln	Val	Arg
465				470				475				480			
Ala	Met	Thr	Tyr	Ser	Gly	Glu	Leu	Lys	Phe	Glu	Lys	Arg	Thr	Ser	Ser
			485				490				495				
Ala	Gln	Val	Glu	Gly	Gly	Val	His	Ser	Leu	His	Ser	Tyr	Glu	Lys	Arg
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Leu	Phe														

<210> 31
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 <222> (67) ... (1611)
 <223> mouse IMP dehydrogenase cDNA double mutant:
 Thr333Ile
 Ser351Tyr

<221> mutation
 <222> 1064
 <223> C to T mutation

<221> mutation
 <222> 1118
 <223> C to A mutation

<400> 31

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	Met	Ala	Asp	Tyr	Leu	Ile	Ser	Gly	Gly	Thr	Ser	Tyr	Val	Pro		
1	5															
gac	gac	ggg	ctc	aca	gcg	cag	cag	ctc	ttc	aac	tgc	ggg	gac	ggc	ctc	156
Asp	Asp	Gly	Leu	Thr	Ala	Gln	Gln	Leu	Phe	Asn	Cys	Gly	Asp	Gly	Leu	
15	20															
acc	tac	aat	gat	ttt	ctc	att	ctt	cct	ggg	tat	atc	gac	ttc	act	gca	204
Thr	Tyr	Asn	Asp	Phe	Leu	Ile	Leu	Pro	Gly	Tyr	Ile	Asp	Phe	Thr	Ala	
35																
gat	cag	gtg	gac	ttg	acg	tct	gct	cta	act	aag	aag	att	aca	cta	aag	252
Asp	Gln	Val	Asp	Leu	Thr	Ser	Ala	Leu	Thr	Lys	Lys	Ile	Thr	Leu	Lys	
50																
acc	cca	ttg	gtt	tcc	tca	ccc	atg	gac	act	gtc	aca	gag	gct	gga	atg	300
Thr	Pro	Leu	Val	Ser	Ser	Pro	Met	Asp	Thr	Val	Thr	Glu	Ala	Gly	Met	
65																
gcc	atc	gcf	atg	gcf	ctt	aca	gga	ggt	att	ggt	ttc	atc	cac	cac	aac	348
Ala	Ile	Ala	Met	Ala	Leu	Thr	Gly	Gly	Ile	Gly	Phe	Ile	His	His	Asn	
80																
tgc	aca	cct	gaa	ttc	cag	gcc	aat	gaa	gtt	cg	aaa	gtg	aag	aaa	tac	396
Cys	Thr	Pro	Glu	Phe	Gln	Ala	Asn	Glu	Val	Arg	Lys	Val	Lys	Lys	Tyr	
95																
gaa	cag	gga	ttc	atc	act	gac	ccc	gtg	gtc	ctt	agc	ccc	aag	gat	cgt	444
Glu	Gln	Gly	Phe	Ile	Thr	Asp	Pro	Val	Val	Leu	Ser	Pro	Lys	Asp	Arg	
115																
gta	cgc	gat	gtt	ttt	gag	gcc	aaa	gcc	agg	cat	ggc	ttc	tgt	ggt	atc	492
Val	Arg	Asp	Val	Phe	Glu	Ala	Lys	Ala	Arg	His	Gly	Phe	Cys	Gly	Ile	
130																
ccc	atc	aca	gat	aca	ggc	cg	atg	ggg	agt	cga	ttg	gtg	ggc	atc	atc	540
Pro	Ile	Thr	Asp	Thr	Gly	Arg	Met	Gly	Ser	Arg	Leu	Val	Gly	Ile	Ile	
145																
tcc	tca	agg	gac	att	gat	ttc	ctc	aag	gag	gaa	gag	cat	gac	cg	ttc	588
Ser	Ser	Arg	Asp	Ile	Asp	Phe	Leu	Lys	Glu	Glu	Glu	His	Asp	Arg	Phe	
160																
ttg	gaa	gag	atc	atg	act	aag	agg	gaa	gat	ttg	gtg	gtc	gcc	cct	gcc	636
Leu	Glu	Glu	Ile	Met	Thr	Lys	Arg	Glu	Asp	Leu	Val	Val	Ala	Pro	Ala	
175																
ggc	gtc	act	ctg	aaa	gag	gca	aat	gag	att	ctg	cag	cga	agt	aaa	aag	684
Gly	Val	Thr	Leu	Lys	Glu	Ala	Asn	Glu	Ile	Leu	Gln	Arg	Ser	Lys	Lys	

195	200	205	
gga aag ttg ccc att gtg aat gaa aat gat gag ctg gta gcc atc att Gly Lys Leu Pro Ile Val Asn Glu Asn Asp Glu Leu Val Ala Ile Ile 210	215	220	732
gcc cgg aca gac cta aag aag aat cgt gat tac ccc ctg gcc tcc aaa Ala Arg Thr Asp Leu Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys 225	230	235	780
gat gcc aag aag caa ctg ctg tgt ggg gca gcc att ggc act cat gag Asp Ala Lys Lys Gln Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu 240	245	250	828
gat gac aag tat agg ctg gac tta ctg gcc ctt gct ggt gtg gat gta Asp Asp Lys Tyr Arg Leu Asp Leu Leu Ala Leu Ala Gly Val Asp Val 255	260	265	876
gtg gtt ttg gac tct tcc cag gga aac tcc atc ttc caa atc aat atg Val Val Leu Asp Ser Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met 275	280	285	924
atc aaa tac atc aag gag aag tat ccc agt cta cag gtc att gga ggc Ile Lys Tyr Ile Lys Glu Lys Tyr Pro Ser Leu Gln Val Ile Gly Gly 290	295	300	972
aat gta gtc act gct gcg caa gcc aag aac ctc ata gat gca ggt gta Asn Val Val Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val 305	310	315	1020
gat gct ttg cga gtc ggc atg gga agt ggt tcc atc tgc atc atc cag Asp Ala Leu Arg Val Gly Met Gly Ser Gly Ser Ile Cys Ile Ile Gln 320	325	330	1068
gaa gtg ttg gcc tgt ggg cgg ccc caa gcc aca gca gtg tac aag gtc Glu Val Leu Ala Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val 335	340	345	1116
tat gag tat gcc cgt cgc ttt ggt gtt cct gtt att gct gat gga gga Tyr Glu Tyr Ala Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly 355	360	365	1164
atc caa aat gtg ggt cat att gcc aaa gct ttg gct ctt ggg gct tcc Ile Gln Asn Val Gly His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser 370	375	380	1212
aca gtc atg atg ggc tcc ctc ctg gct gcc acc act gag gcc cct ggc Thr Val Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly 385	390	395	1260
gag tac ttc ttc tca gat ggg atc cgg ctg aag aaa tac cga ggt atg Glu Tyr Phe Phe Ser Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met 400	405	410	1308
ggt tct ctt gat gcc atg gac aaa cat ctc agc agc cag aac cga tac Gly Ser Leu Asp Ala Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr 415	420	425	1356
ttc agt gaa gct gac aaa atc aaa gtg gcc caa gga gtt tca ggg gca Phe Ser Glu Ala Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala 435	440	445	1404
gtg cag gac aag ggg tct atc cac aag ttc gtt cct tac ctg att gct Val Gln Asp Lys Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala 450	455	460	1452
ggc atc cag cat tcc tgt caa gac att ggt gcc aag agt tta acc caa			1500

Gly Ile Gln His Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln			
465	470	475	
gtc aga gcc atg acg tac tcg ggg gag ctt aaa ttt gag aag agg aca		1548	
Val Arg Ala Met Thr Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr			
480	485	490	
tcc tct gct cag gtg gaa ggt ggc gtc cac agc ctc cat tcg tac gag		1596	
Ser Ser Ala Gln Val Glu Gly Val His Ser Leu His Ser Tyr Glu			
495	500	505	510
aaa cgg ctt ttc tga aaacagatcc agtataatgcc ttgaattttt caataaaaagt		1651	
Lys Arg Leu Phe *			
ttggggaaaaaa aaaagtgaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaa		1707	
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<211> 514			
<212> PRT			
<213> Mus musculus			
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1 5 10 15			
Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr			
20 25 30			
Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln			
35 40 45			
Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro			
50 55 60			
Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile			
65 70 75 80			
Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr			
85 90 95			
Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln			
100 105 110			
Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg			
115 120 125			
Asp Val Phe Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile			
130 135 140			
Thr Asp Thr Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser			
145 150 155 160			
Arg Asp Ile Asp Phe Leu Lys Glu Glu His Asp Arg Phe Leu Glu			
165 170 175			
Glu Ile Met Thr Lys Arg Glu Asp Leu Val Val Ala Pro Ala Gly Val			
180 185 190			
Thr Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys			
195 200 205			
Leu Pro Ile Val Asn Glu Asn Asp Glu Leu Val Ala Ile Ile Ala Arg			
210 215 220			
Thr Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ala			
225 230 235 240			
Lys Lys Gln Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp			
245 250 255			
Lys Tyr Arg Leu Asp Leu Leu Ala Leu Ala Gly Val Asp Val Val Val			
260 265 270			
Leu Asp Ser Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys			
275 280 285			
Tyr Ile Lys Glu Lys Tyr Pro Ser Leu Gln Val Ile Gly Gly Asn Val			
290 295 300			
Val Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala			
305 310 315 320			
Leu Arg Val Gly Met Gly Ser Gly Ser Ile Cys Ile Ile Gln Glu Val			
325 330 335			
Leu Ala Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Tyr Glu			
340 345 350			

Tyr Ala Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln
 355 360 365
 Asn Val Gly His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val
 370 375 380
 Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr
 385 390 395 400
 Phe Phe Ser Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser
 405 410 415
 Leu Asp Ala Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser
 420 425 430
 Glu Ala Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln
 435 440 445
 Asp Lys Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile
 450 455 460
 Gln His Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg
 465 470 475 480
 Ala Met Thr Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser
 485 490 495
 Ala Gln Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg
 500 505 510
 Leu Phe

<210> 33

<211> 5627

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Sequence of pMG
plasmid from InvivoGen

<400> 33

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 ttgatgagtt tggacaaacc acaaactagaa tgcagtgaaa aaaatgcttt atttgtgaaa 120
 tttgtgatgc tattgcttta tttgtgaaat ttgtgatgct attgctttat ttgttaaccat 180
 tataagctgc aataaaacaag ttaacaacaa caattgcatt cattttatgt ttcaggttca 240
 gggggaggtg tggaggttt tttaaagcaa gtaaaacctc tacaaatgtg gtagatccat 300
 ttaaatgtta attaagaaca tgtgagcaaa aggccagcaa aaggccagga accgtaaaaaa 360
 ggccgcgttg ctggcggtt tccataggtc ccgcggccct gacgagcatc acaaaaatcg 420
 acgctcaagt cagaggtggc gaaacccgac aggactataa agataccagg cgtttcccc 480
 tggaaagctcc ctcgtgcgtc ctccgttcc gaccctgccc cttaccggat acctgtccgc 540
 ctttctccct tcgggaagcg tggcgcttc tcatagctca cgctgttaggt atctcagttc 600
 ggttaggtc gttcgctcca agctggctg tgtgcacgaa ccccccgttc agcccgaccg 660
 ctgcgcctta tccggttaact atcgtcttga gtccaaacccg gtaagacacg acttatcgcc 720
 actggcagca gccactggta acaggattag cagagcgagg tatgttaggcg gtgctacaga 780
 gtttttgaag tggggccta actacggcta cactagaaga acagtatttgc gtatctgcgc 840
 tctgctgaag ccagttaccc tcggaaaaag agttggtagc tcttgatccg gcaaacaac 900
 caccgctggc agcgggtggc tttttgtttt caagcagcag attacgcgc gaaaaaaaaagg 960
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 gactttctta cttggcagta catctacgta ttagtcatcg ctattaccat ggtgatgcgg 1560
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 gggtatgtgt ctgaaaatga gctcgggag cgggcttgca ccgctgacgc atttggaa 2520
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 ctgttctgccc ccgttacaga tccaagctgt gaccggcgcc tacgtaaatg atatctacta 5520
 gatttatcaa aaagagtgtt gacttgcgt gctcacaat tgatacttag attcatcgag 5580
 agggacacgt cgactactaa cttcttctc tttcctacag ctgagat 5627

<210> 34

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Forward primer for amplification-

based cloning of hIMPDH type II cDNA

<400> 34
gctatctgca ggccgccacc atggccgact acctgattag 40

<210> 35
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Reverse primer for amplification-based cloning of hIMPDH type II cDNA

<400> 35
catactttc gccaaaaaga ctagatctcg atc 33

<210> 36
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Forward primer for T333I mutation of hIMPDH type II cDNA

<400> 36
ggctccatct gcattatcca ggaagtgctg gc 32

<210> 37
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Reverse primer for T333I mutation of hIMPDH type II cDNA

<400> 37
ccgaggtaga cgtaataggt cttcacgac cg 32

<210> 38
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Forward primer for S351Y mutation of hIMPDH type II cDNA

<400> 38
cagcagtgtca aagggttat gatgcac ggcgttt 38

<210> 39
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Reverse primer for S351Y mutation of hIMPDH type II cDNA

<400> 39
 gtcgtcacat gttccacata ctcatacgtg ccgcgaaac 39

<210> 40
 <211> 8238
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> (54) ... (1598)
 <223> Nucleotide sequence of plasmid IMPDH(I)Hytk/pMG⁺Pac containing DNA
 encoding an altered human IMPDH (T333I/S351Y) within plasmid pMG

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 Met
 1

gcc gac tac ctg att agt ggg ggc acg tcc tac gtg cca gac gac gga 104
 Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp Gly
 5 10 15

ctc aca gca cag cag ctc ttc aac tgc gga gac ggc ctc acc tac aat 152
 Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr Asn
 20 25 30

gac ttt ctc att ctc cct ggg tac atc gac ttc act gca gac cag gtg 200
 Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln Val
 35 40 45

gac ctg act tct gct ctg acc aag aaa atc act ctt aag acc cca ctg 248
 Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro Leu
 50 55 60 65

gtt tcc tct ccc atg gac aca gtc aca gag gct ggg atg gcc ata gca 296
 Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile Ala
 70 75 80

atg gcg ctt aca ggc ggt att ggc ttc atc cac cac aac tgt aca cct 344
 Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr Pro
 85 90 95

gaa ttc cag gcc aat gaa gtt cgg aaa gtg aag aaa tat gaa cag gga 392
 Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Glu Gln Gly
 100 105 110

ttc atc aca gac cct gtg gtc ctc agc ccc aag gat cgc gtg cg gat 440
 Phe Ile Thr Asp Pro Val Val Leu Ser Pro Lys Asp Arg Val Arg Asp
 115 120 125

gtt ttt gag gcc aag gcc cgg cat ggt ttc tgc ggt atc cca atc aca 488
 Val Phe Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile Thr
 130 135 140 145

gac aca ggc cgg atg ggg agc cgc ttg gtg ggc atc atc tcc tcc agg 536
 Asp Thr Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser Arg
 150 155 160

gac att gat ttt ctc aaa gag gag gaa cat gac tgt ttc ttg gaa gag 584
 Asp Ile Asp Phe Leu Lys Glu Glu His Asp Cys Phe Leu Glu Glu
 165 170 175

ata atg aca aag agg gaa gac ttg gtg gta gcc cct gca ggc atc aca 632
 Ile Met Thr Lys Arg Glu Asp Leu Val Val Ala Pro Ala Gly Ile Thr
 180 185 190

ctg aag gag gca aat gaa att	ctg cag cgc agc aag aag gga aag ttg	680	
Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys Leu			
195	200	205	
ccc att gta aat gaa gat gat gag ctt gtg gcc atc att gcc cg aca	728		
Pro Ile Val Asn Glu Asp Asp Glu Leu Val Ala Ile Ile Ala Arg Thr			
210	215	220	225
gac ctg aag aag aat cgg gac tac cca cta gcc tcc aaa gat gcc aag	776		
Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ala Lys			
230	235	240	
aaa cag ctg ctg tgt ggg gca gcc att ggc act cat gag gat gac aag	824		
Lys Gln Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp Lys			
245	250	255	
tat agg ctg gac ttg ctc gcc cag gct ggt gtg gat gta gtg gtt ttg	872		
Tyr Arg Leu Asp Leu Leu Ala Gln Ala Gly Val Asp Val Val Val Leu			
260	265	270	
gac tct tcc cag gga aat tcc atc ttc cag atc aat atg atc aag tac	920		
Asp Ser Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys Tyr			
275	280	285	
atc aaa gac aaa tac cct aat ctc caa gtc att gga ggc aat gtg gtc	968		
Ile Lys Asp Lys Tyr Pro Asn Leu Gln Val Ile Gly Gly Asn Val Val			
290	295	300	305
act gct gcc cag gcc aag aac ctc att gat gca ggt gtg gat gcc ctg	1016		
Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala Leu			
310	315	320	
cg ggt ggc atg gga agt ggc tcc atc tgc att atc cag gaa gtg ctg	1064		
Arg Val Gly Met Gly Ser Gly Ser Ile Cys Ile Ile Gln Glu Val Leu			
325	330	335	
gcc tgt ggg cgg ccc caa gca aca gca gtg tac aag gtg tat gag tat	1112		
Ala Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Tyr Glu Tyr			
340	345	350	
gca cgg cgc ttt ggt gtt ccg gtc att gct gat gga gga atc caa aat	1160		
Ala Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln Asn			
355	360	365	
gtg ggt cat att gcg aaa gcc ttg gcc ctt ggg gcc tcc aca gtc atg	1208		
Val Gly His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val Met			
370	375	380	385
atg ggc tct ctc ctg gct gcc acc act gag gcc cct ggt gaa tac ttc	1256		
Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr Phe			
390	395	400	
ttt tcc gat ggg atc cgg cta aag aaa tat cgc ggt atg ggt tct ctc	1304		
Phe Ser Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser Leu			
405	410	415	
gat gcc atg gac aag cac ctc agc agc cag aac aga tat ttc agt gaa	1352		
Asp Ala Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser Glu			
420	425	430	
gct gac aaa atc aaa gtg gcc cag gga gtg tct ggt gct gtg cag gac	1400		
Ala Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln Asp			
435	440	445	
aaa ggg tca atc cac aaa ttt gtc cct tac ctg att gct ggc atc caa	1448		
Lys Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile Gln			
450	455	460	465

cac tca tgc cag gac att ggt gcc aag agc ttg acc caa gtc cga gcc	1496
His Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg Ala	
470	475
480	
atg atg tac tct ggg gag ctt aag ttt gag aag aga acg tcc tca gcc	1544
Met Met Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser Ala	
485	490
495	
cag gtg gaa ggt ggc gtc cat agc ctc cat tcg tat gag aag cgg ctt	1592
Gln Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg Leu	
500	505
510	
ttc tga tctagctcga catgataaga tacattgatg agtttggaca aaccacaact	1648
Phe *	

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